78224 STIC-Biotech/ChemLib

9-183

200714

Maj

From:

Seharaseyon, Jegatheesan

Sent:

Wednesday, September 06, 2006 10:29 AM

To:

STIC-Biotech/ChemLib

Subject:

Re: 10/659684

Hi,

Please search SEQ ID NO: 2 ansd 115 of 10/659684 in the commercial database.

Thanks.

Seyon.

J. Seharaseyon Remsen 4C61, Box 4C70.

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed: 9-7-00
Searcher Prep Time:
Online Time:

Type of Search

NA#______ AA#:_____

S/L:____ Oligomer:_____
Encode/Transl:_____

Structure #:____ Text:___

Inventor:_____ Litigation:____

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
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tumourigenesis;

zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma; tumourigenesis; leukaemia; hematopoiesis; B cell tumour.

A human zalphall ligand

polypeptide.

22-JAN-2001 AAB18623;

(first entry)

AAB18623 standard; protein;

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ALIGNMENTS

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09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                 New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and in vivo, and for treating tumorigenesis.
                                                                                             WPI; 2000-565600/52.
N-PSDB; AAA75552.
                                                                                                                 Novak JE, Presnell SR, Gross JA, Johnston JV,
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99US-00265992.
99US-0142013P.
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Nelson AJ, I
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The present sequence represents a human zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of heaptopietic cells in vitro and in vivo. Zalphall ligand polymucleotides can be used as primers or probes for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for

Disclosure; Page 205-206; 256pp; English.

treating

leukaemias and

lymphomas. Antagonists against zalphall ligand

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis,
                05-APR-2000; 2000US-0194731P.
28-JUL-2000; 2000US-0222121P.
                                                                   03-APR-2001; 2001WO-US010872.
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ilarity 100.0%;
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                                                                                                                                                                                                          Location/Qualifiers
                                                                                     /label= Mature_zalphall_Ligand
                                                                                                                                                   /label= Signal_peptide
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Pred. No. 2e-86;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of a novel cytokine, CC zalphall Ligand and the polynucleotide encoding it. The invention also CC gives the sequence for the zalphall receptor and the polynucleotide CC encoding it. The zalphall Ligand polypeptide stimulates proliferation of CC natural killer (NK) cells or NK cell progenitors, the activation of NK CC cells, proliferation of T-cells, proliferation of B-cells stimulated with CC cells, proliferation of B-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The CC zalphall Ligand polypeptide is also useful in preparing antibodies that CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, CC and in gene therapy. Zalphall Ligand may also be used to identify CC inhibitors of its activity, to enhance the generation of anti-tumour CC responses with or without the infusion of donor lymphocytes, and to CC activate or stimulate the immune system. The present sequence represents human zalphall Ligand polypeptide. The cDNA encoding this is isolated CC from a cDNA library from activated human peripheral blood cells (hPBCS)
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Best Local
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11-MAR-1999;
01-JUL-1999;
arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R; immune cell activity; cancer; infectious disorder; antirheumatic; antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacteri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gross JA,
                                                                                                                           Human IL-21 SEQ ID NO:19
                                                                                                                                                                                                                                                                                                                  ABR61407 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162
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99US-0123904P.
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Nelson AJ, Dillon SR, 1
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      cytostatic; antibacterial;
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MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF

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Matches Query Match

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Score 850; DB 6 Pred. No. 2e-86; Mismatches

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Length Indels

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Gaps

Sequence 162 AA;

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virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological; neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic; antithyroid; antiinflammatory; immune response; immune disorder; autoimmune disease; human.
                                                                                                                                                                                                             Treating or preventing arthritic disorder, cancer or infectious disorders in a subject, involves administering a modulator of interleukin-21 or its receptor which modulate immune cell activity.
                                                                                                                                                                                                                                                               Carter L, Whi Donaldson DD,
                                                                                                                                                                                                                                                                                             04-OCT-2001; 2001US-00972218
17-APR-2002; 2002US-0373746P
                                                                                                                                                                                                  Disclosure; Page 37; 176pp; English.
                                                                                                                                                                                                                                       WPI; 2003-430146/40.
N-PSDB; ACC80873.
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                                                                                                                                                                                                                                                               Collins M,
Dunussi K,
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Ma M,
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Witek JS, Kasaian MT;
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The invention relates to polynucleotides and polypeptides of interleukin-
21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
that is not detectable in receptor binding studies. The antagonists of
the invention have mutations in the D helix of the IL-21 molecule, and
can be used to inhibit the activity of IL-21 with its cognate receptor.
                                                                                                                                                                                                                         New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-21; IL-21; antagonist; cancer; inflammatory; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; humzalphall ligand.
                                                                                                                                                   Disclosure; Page 53-54; 71pp; English
                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-441547/41.
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28-APR-2000;
11-MAY-2000;
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                      New fusion polypeptide for regulating hematopoiesis and immune responses, comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; MU-1; haematopoietin receptor superfamily chain; immunom cytostatic; antibacterial; virucide; antianaemic; gene therapy; haematopoiesis; anaemias; immune response; cancer; infection;
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(WHIT/) WHITTERS M J.
(COLL/) COLLINS M.
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DB; ACD26729.
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) DONALDSON D
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) UNGER M.
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Pred. No. 2e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic; antiinflammatory; dermatological; ophthalmological; uropathic; muscular-gen; vasotropic; antidiabetic; antithyroid; thyromimetic; neuroprotective; gastrointestinal-gen; antipsoriatic; gene therapy.
                                                                                                                        New substantially pure interleukin-21 polypeptide, useful for diagnosing treating and prognosticating autoimmune disorders, e.g. rheumatic disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis and myasthenia gravis.
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                                                                                                                                                                                                                                                                                                                                               Moll T,
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                                                          65pp; English.
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Pred. No. 2e-86;
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CC include mutants of murine IL-21 in which the Gln residue at position 119
CC residues at positions 114 and 119 of the mature polypeptide are both
CC replaced by Asp. The mutant IL-21 golypeptides inhibit or suppress T-cell
CC activation. They preferably comprise a sequence that increases
CC circulating half-life, such as the Fc region of an IgG molecule and may
CC further comprise an antigenic tag. Such antagonists inhibit cellular
CC proliferation in response to either anti-CD3 monoclonal antibodies or
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
CC IL-21. A claimed method of suppressing the immune response in a patient
CC comprises administering the IL-21 antagonist or a nucleic acid encoding
CC it. The method is used to treat an autoimmune disease such as rheumatic
CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
CC arthritis, type I disabetes, autoimmune disease of the thyroid such as
CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the chyroid such as
CC encephalomyelitis, or an autoimmune disease selected from pemphigus
CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,
CC Batazilian pemphigus, psoriasis or inflammatory bowel disease (all
                        Query Match
Best Local :
Matches 162;
                                                                                                   Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21). The invention provides antagonists of the IL-21 receptor. These include mutants of murine IL-21 in which the Gln residue at position
                          Similarity
  Conservative
                     100.0%;
0:
                          Score 850; DB 7
Pred. No. 2e-86;
  Mismatches
                                                ٠7;
                                                Length 162;
  Indels
  <u>..</u>
  Gaps
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                                                                              LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                          MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60
              TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
                                                           LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
                                                                                                                           MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                120
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RESULT 8
ADF17046
21-DEC-2001;
24-JAN-2002;
28-JAN-2002;
26-FEB-2002;
                                                                                                                                                                      albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human; gene; ds.
                                                                                                                                                                                                                                   12-FEB-2004
                 28-FEB-2002;
27-MAR-2002;
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                          ADF17046 standard;
         08-APR-2002;
                                                                                        23-DEC-2002;
                                                                                                                              WO2003060071-A2
                                                                                                                                                                                                             Human albumin fusion protein-related protein SeqID2177.
                                    2001US-0341811P.
2002US-0350358P.
2002US-0351360P.
2002US-0359370P.
                                                                                                                                                                                                                                   (first entry)
          2002US-0367500P.
2002US-0370227P.
                                                                                        2002WO-US040891.
                              2002US-0360000P.
                                                                                                                                                                                                                                                                          protein; 162
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The present sequence is the protein sequence of human interleukin-21 (IL-

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                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel albumin fusion protein having albumin CC or biological activity. Human serum albumin is responsible for a CC significant proportion of the osmotic pressure of serum and also CC functions as a carrier of endogenous and exogenous ligands. The fusion of CC the therapeutic protein may increase shelf-life and stability of CC albumin to a therapeutic protein may increase shelf-life and stability of CC allow production of compositions with antidiabetic activity whilst the CC nucleotide sequence which encodes it may be useful for gene therapy. The CC albumin fusion protein is useful for preparing a composition for treating CC diabetes mellitus. The present sequence is that of a therapeutic protein CC which was fused with human albumin to create a novel albumin fusion CC protein of the invention. Note: The sequence data for this patent did not CC form part of the printed specification, but was obtained in electronic CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                              Matches 162;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2002;
09-AUG-2002;
13-AUG-2002;
18-SEP-2002;
18-SEP-2002;
02-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2002;
28-MAY-2002;
05-JUN-2002;
10-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New albumin fusion protein, useful for preparing a composition treating diabetes mellitus.
 Human; Zalphall ligand; Zalphall receptor; immune response;
                             Human Zalphall ligand protein
                                                                                       ADH44572
                                                                                                                  ADH44572 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162
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DELTA BIOTECHNOLOGY I
PRINCIPIA PHARM CORP.
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                                                                                                                                                                                                                                                                 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                   MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60
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2002US-0385708P
2002US-0394625P
2002US-0398008P
2002US-0402131P
2002US-0402708P
2002US-0411355P
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; 2002US-0414984P.
; 2002US-0417611P.
; 2002US-0420246P.
; 2002US-0423623P.
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                        (first entry)
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Pred. No. 2e-86;
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                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                          162;
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Novak JE,
Gross JA,
                                                                                                 Stimulating an immune response in a mammal exposed to an pathogen, useful for enhancing anti-tumor activity result tumor progression or metastasis, comprises administering
                                                                                                                                                                                                                                                                                                                          09-MAR-1999; 99US-0123547P.
11-MAR-1999; 99US-0123904P.
01-JUL-1999; 99US-0142013P.
09-MAR-2000; 2000US-00522217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour progression; metastasis; tumour stasis; haematopoietic lymphoma; B cell tumour; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; diabetes; infectious immunocompromised patient; HIV infection; vaccine; chromosome
                                        Claim 1; SEQ ID NO 2; 103pp; English.
                                                                                polypeptide.
                                                                                                                                                                                     WPI; 2003-895283/82.
                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2001; 2001US-00923246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                           Presnell
Johnston
relates to stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                             JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mature Zalphall,
                                                                                                                                                                                                                           Sprecher CA, Foster D
Nelson AJ, Dillon SR,
    an immune
                                                                                                                                                                                                                Foster DC, horr, SR, Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claimed in
    response
                                                                                                                        resulting in red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim
    in a mammal
                                                                                                     ting İn reduced
zalphall ligand
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CC The invention relates to stimulating an immune response in a mammal cexposed to an antigen or pathogen comprises administering a composition comprising mature zalphall ligand polypeptide comprising residues 32-162 cc fADH44572 in a pharmaceutical vehicle. Also included are stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining (in) directly the level of antigen or pathogen (comprising the lateral polypeptide in a pharmaceutical vehicle; (c) determining (in) directly the level of antigen or pathogen in the mammal; (b) administering a composition comprising in the antigen or pathogen in the mammal; (c) and (d) comparing the antigen or pathogen level in (a) with (b), where a composition of immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining a level of antigen- or pathogen- comprising: (a) determining a level of antigen- or pathogen- general polypeptide in a pharmaceutical vehicle; (c) determining a post (d) comparing the level of the antigen- or pathogen- specific antibody; (d) administering a composition comprising ralphall composition the antibody level indicates stimulation of immune response). The method is useful for stimulating an immune response in a mammal composed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, or all cell tumour. The zalphall ligand is useful for treating a wide range of diseases arising from defects in the immune system, e.g. crasse of diseases arising from defects in the immune system, e.g. crasses of the present sequence is a human Zalphall ligand in improving communication. The present sequence is a human Zalphall ligand protein.

Sequence 162 AA;

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Query Match 100.0%; Score 850; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
AD10098
ID AD1000
XX AD100
XX AD100
XX AD100
XX Zalph
XW Zalph
XW Zalph
XW HIV;
XX HOW
PN US200
XX US200
XX US200
XX HOMO
XX HOMO
XX HOMO
PN US201
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XX HOYA)
PI Gross
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DR N-PSI
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                                                                                                                                                                                      Query Match
Best Local S
Matches 162
                                                                                                                                                                                                                                                                              The invention relates to a novel isolated zalphall ligand polypeptide. The polypeptide of the invention may be useful for boosting immunity to infectious diseases and treating immunocompromised patients, such as HIV patients, as well as in improving vaccines. The current sequence is that of the human zalphall ligand protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                      New zalphall ligand polypeptides, useful for boosting immunity to infectious diseases, and treating immunocompromised patients, such as human immunodeficiency virus (HIV) patients, or in improving vaccines.
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                         Claim 7; SEQ ID NO 2; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-811003/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2002; 2002US-00295723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zalphall ligand; immunity; infectious disease; immunocompromised patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
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 121
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                                                                                                                                                                                                      Similarity
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                      TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
                                                                               LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                          MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60
                                                                                                                                                                                                                                                    162 AA;
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                                                             LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
                                                                                                                        MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
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TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
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Johnston JV,
                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative 0
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Nelson AJ, Dillon SR,
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                                                                                                                                                                                   Score 850; DB 7;
Pred. No. 2e-86;
); Mismatches 0;
                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                   Length 162;
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                                                                                                                                                                                      Gaps
                                                             120
                                                                                                                        60
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MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF

Conservative

0

Score 850; DB 8 Pred. No. 2e-86; Mismatches

Indels

<u>.</u>

Gaps

0

6 60

8; 0

100.0%;

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RESULT 11
ADH10501
                                                                                                       The invention relates to treating Non-Hodgkin's lymphoma, cancer or CC infection and involves administering to the subject a polypeptide having CC a functional activity of interleukin-21 (IL-21). The methods are useful CC epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and CC epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and CC colon cancer; viral infection such as AIDS, Hepatitis B or C virus, CC gastroenteritis, haemorrhagic diseases, anteritis, carditis, carcer and CC encephalitis, paralysis, brochholitis, upper or lower respiratory CC disease, respiratory papillomatosis; arthritis, disseminated disease, CC meningitis, and mononucleosis; or bacterial infection, such as an CC infection by a bacterial selected from chlamydiae, listeriae, helicobacter CC pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden CC viruses, Epstein-Barr virus, Cytomegalovirus, Pox viruses, Papilloma CC viruses, Epstein-Barr virus, Ortomegalovirus, Pox viruses, Papilloma CC viruses, Adenovirus, Poliovirus, Ortomegalovirus, Pox viruses, Papilloma CC viruses, Adenovirus, Poliovirus, Ortomegalovirus, Pox viruses, Papilloma Viruses, caliciviruses, rables viruses, and rinderpest viruses. CC The present sequence represents a human IL-21 polypeptide.
Query Match
Best Local Similarity
Matches 162; Conserv
                                                                            Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating Non-Hodgkin's lymphoma, cancer or infection comprises administering to the subject a polypeptide having a functional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADH10500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2002; 2002US-0387127P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2003; 2003WO-US017808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatotropic; neuroprotective; muscular; respiratory; antiarthritic; antibacterial; anti-HIV; gene therapy; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin-21 (IL-21) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH10501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH10501 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; SEQ ID NO 2; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-062206/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "specifically claimed fragment"
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RESULT 12
ADJ25621
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                           The present invention describes a method for inhibiting interferon gamma (IFNgamma) levels in a T cell population by contacting the T cell or cell coppulation with an interleukin 21 (II-21) agonist in an amount sufficient to inhibit IFNgamma in the T cell or cell population, wherein the agonist is an II-21 polypeptide comprising an amino acid sequence at least 85% identical to the 162 amino acids (SEQ ID NO: 2, ADJ25621), and which is capable of binding to an II-21R. An II-21 agonist has antiasthmatic, antiallergic, antiarthritic, antirheumatic, neuroprotective, antiinflammatory, dermatological, immunosuppressive, muscular and cantingsoriatic activities. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of II-21, T helper 1 (Thl) and/or Th2, such as asthma, allergy, rheumatoid arthritis, multiple sclerosis, lupus, diabetes, Crohn's disease, peoriasis and myasthenia gravis. The present sequence represents human II composition of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL-21 agonist; antiasthmatic; antiallergic; antiarthritic; antirheumatic; neuroprotective; antiinflammatory; dermatological; immunosuppressive; muscular; antiporiatic; Thelper; Thi, Th2; asthma; allergy; rheumatoid arthritis; multiple sclerosis; lupus; diabetes; Crohn's disease; psoriasis; myasthenia crewin.
                                                                                                                                                                                                                                                                                                                                                                Inhibiting interferon gamma (IFNgamma) levels and T helper cell development and function in a T cell or cell population using II-21 modulators, useful for the preventing and/or treating asthma, allergy, arthritis, lupus and diabetes.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-122921/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002; 2002US-0396160P
12-AUG-2002; 2002US-0403001P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin 21 (IL-21) protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ25621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2003; 2003WO-US021975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HARVARD COLLEGE.
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 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wurster A,
ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
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Query Match Best Local Similarity

100.

. 0 %

Score Pred.

850; DB 8; No. 2e-86;

Length

Query Match

100.0%;

Score

850;

DB 8

Length 162;

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RESULT 13
ADM41017
ID ADM41
XX ADM41
XX ADM41
XX ADM41
XX ADM41
XX Antig
KW Antig
COS Homo
XX Homo
XX Homo
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PR 11-00
PR 11-
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                                                                                 The invention relates to an interleukin (IL)-21 that is used for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases. Methods of the invention are useful for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, such as allergic conditions (e.g. asthma, allergic rhinitis or allergic diseases of the skin) and/or parasitic diseases, aspecially helminthic infection. The current sequence represents the DNA sequence encoding IL-21. Note: This sequence is not encoded by that of ADM41016, which we are told in the specification is the IL-21 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2002; 2
16-OCT-2002; 2
17-OCT-2002;
Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of Interleukin-21 for the treatment of diseases or eosinophils are involved in a protective response in a allergic conditions and/or parasitic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anthelmintic; dermatological; immunomodulator; interleukin;
eosinophil; allergic; parasitic; asthma; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 2; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-340821/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Romer J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-2003; 2003WO-DK000691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IL-21 amino acid sequence, seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM41017
                                                          nucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moller NPH,
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2002DK-00001587.
2002US-0419225P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subject, e.g.
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Best Local Similarity

100.0%;

Pred. No. 2e-86;

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RESULT 14
ADP12563
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   Query Match 100.0%; Best Local Similarity 100.0%; Matches 162; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                     The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or vital, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth J, Rosenberg S;
                                                                                                                     Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 65; SEQ ID NO 2572; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-400724/37
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20-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by mRNA of the invention #173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplant rejection; immune inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EXPR-) EXPRESSION DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes.
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2002US-00325899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fry K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system;
sease; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Woodward R,
Score 850; DB w;
Pred. No. 2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid
sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis; lupus; HIV; AIDS.
                                                               Length 162;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morris
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Gaps

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RESULT 15
ADP19731
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XX ADP199
XX ADP199
XX ADP190
XX ADP1
The invention describes an isolated polypeptide comprising a sequence of CC amino acid residues that is at least 90 or 95% identical to residues 41 CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the CC specification. Also described are: a pharmaceutical composition CC comprising the polypeptide, and a vehicle; a method of treating cancer in CC a mammal; a method of stimulating an immune response in a mammal with CC at the cancer in a mammal and the composition comparising a method of stimulating an immune response in a mammal bearing CC attnour; an isolated polynucleotide comprising a sequence of nucleotides that encode amino acid residues cited above, where the polynucleotide (CC encodes a polypeptide that binds a receptor comprising 538 amino acids, CC fully defined in the specification; a pharmaceutically acceptable composition the polynucleotide encoding, in a pharmaceutically acceptable composition at a control element, and a DNA segment comprising the following operably linked compositions and an isolated polynucleotide molecule comprising at least 10 nucleotides of the polynucleotide sequence of 642 bp, fully defined in the specification. The molecules, compositions and methods are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novak JE,
Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADP19730, ADP19732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; zalpha11 ligand; pharmaceutical; cancer; immune response;
melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New zalphall ligand polynucleotide and polypeptide molecules, useful for treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 2; 111pp;
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99US-0142013P.
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Nelson AJ, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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Title:
Perfect score:
Sequence:
                  Scoring table:
                                                                                                                                                           Run on:
                                                                                                                                                                                         OM protein - protein search, using
                                                    US-10-659-684-2
850
1 MRSSPGNMERIVIC
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                         September 7, 2006, 12:45:21; Search time 11.8029 Seconds
                                                    MRSSPGNMERIVICLMVIFL.....
                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                              GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                           sw model
                                                                                                                        (without alignments) 1320.622 Million cel
                                                       LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                       cell updates/sec
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum Maximum DB seq length: 0
DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	ហ	4.	ω	2	1	Result No.	
73.5.	73.5	73.5	73.5	٠			73.5	73.5	74	74	74	74.5	74.5	74.5	74.5	75	75.5	75.5	75.5	76	76.5	76.5	78	79	82	83	91.5	94.5	Score	
8.6	8.6	:	8.6		8.6	8.6		8.6	8.7	8.7	8.7	8.8	8.8	8.8	8.8	8.8	8.9	8.9	8.9	8.9	9.0	9.0	9.2	9.3	9.6	9.8	10.8	11.1	Query Match	40
2118	868	565	484	484	477	472	447	162	2197	953	440	848	789	482	286	321	1206	406	336	195	864	420	741	206	607	899	567	162	Length	
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T13612	T31527	G89878	A46608	S39315	S21049	159087	S39316	149124	B71600	I48078	T47906	T00372	844759	841211	F82881	T46352	S24407	T28957	S42632	S42022	S60441	A25876	JC7822	S49882	ABXL72	B38529	S29498	A53484	ID	
hypothetical prote	hypothetical prote	conserved hypothet	voltage-dependent	CAB3a protein - hu	calcium channel pr	ISG-K54 - human	CAB3b protein - hu	interleukin-15 - m	variant-specific s	CHO1 antigen - Chi	FUSCA PROTEIN FUS6	hypothetical prote	C14B9.5 protein -				н	hypothetical prote	Fit-1S protein pre	lycola	prot			hypothetical prote	74K albumin precur	Η		leukir	ion	•

RESULT 2 S29498

Tymphocyte antigen Ly84 precursor - mouse
N;Alternate names: 38.5K T1 glycoprotein; ST2L protein
C;Species: Mus musculus (house mouse)
C;Date: 13.7an-1995 #Bequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29498; A33541; S17657; S07054
R;Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tominaga, S.
FEBS Lett. 318, 83-87, 1993
A;Title: Presence of a novel primary response gene ST2L, encoding a product highly simil.
A;Reference number: S29498; MUID:93170492; PMID:7916701
A;Accession: S29498
A;Acce

A;Cross-references: UNIPROT:P14719; UNIPARC:UPI0000029617; EMBL:D13695; NID:g286100; PID:R;Klemenz, R.; Hoffmann, S.; Werenskiold, A.K.

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421 484 674	262 546 719	667 1101 257 262	234 304 1291 309 380
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C84555 S62185 S61181	T41813 G72210 T27977 T43445	D96923 T26919 C69230 F72858	G97966 A32108 T22382 T41889 T25454
hypothetical prote calcium channel be hypothetical prote	AcMNPV or169 - Bom hypothetical prote lin-15A protein - hypothetical prote	pot hyl	hypothetical prote translation:initia hypothetical prote PB38 orf153 - Bomb hypothetical prote

ALIGNMENTS

\$ Q B	Query Best L Matche	A; Molecu A; Molecu A; Residu A; Cross- A; Note: C; Superf C; Keywor F; 49-162 F; 83-133	A;Reference A;Accession:	RESULT 1 A53484 interleu C;Specie C;Date: C;Access R;Grabst
51 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISHESGDTDIHD 109 94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149 ;	Query Match 11.1%; Score 94.5; DB 1; Length 162; Best Local Similarity 25.9%; Pred. No. 0.19; Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5; 43 IDIVDQLKNYVNDLVPEFLPAPEDYETNCEWSAFSCFQKAQLKSANTGNNE 93	A;Status: nucleic acid sequence not shown A;Nolecule type: mRNA A;Residues: 1-162 <gra> A;Residues: 1-162 <gra> A;Rose-references: UNIPROT:P40221; UNIPARC:UPI0000031AC6; GB:U03099; NID:9493521; PIDN:A;Roce: the complete translation is not shown C;Superfamily: interleukin-15 C;Ruperfamily: interleukin-15 #status predicted <mat> F;49-162/Product: interleukin-15 #status predicted <mat> F;83-133,90-136/Disulfide bonds: #status predicted</mat></mat></gra></gra>	Science 264, 965-968, 1994 Science 264, 965-968, 1994 A;Title: Cloning of a T cell growth factor that interacts with the beta chain of the int- A;Reference number: A53484; MUID:94233380; PMID:8178155 A;Accession: A53484	RESULT 1 A53484 A53484 Interleukin-15 precursor - green monkey C;Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A53484 C;Accession: A53484 A;Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Beer

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Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A;Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to A;Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to A;Reference number: A33541
A;Recession: A33541
A;Recession: A33541
A;Molecule type: mRNA
A;Residues: 1-191,'V',193-328,'SKECPSHIA' <KLE>
A;Cross-references: UNIPARC:UPI000028A98; GB.M24843; NID:g201103; PIDN:AAA40160.1; PID: A;Cross-references: UNIPARC:UPI000028A98; GB.M24843; NID:g201103; PIDN:AAA40160.1; PID: R;Tominaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991
A;Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal mapper approximate the murine ST2 gene. Teachers and Chromosomal mapper approximate the murine ST2 gene. Characterization and chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene. Characterization and Chromosomal mapper approximate the murine ST2 gene.
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A;Map position: 1
A;Map position: 1
A;Introns: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2
A;Introns: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2
C;Superfamily: interleukin-1 receptor type I
C;Keywords: glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-26/Domain: signal sequence #status predicted <MAT>
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A;Residues: 1-328,'SKECPSHIA' <TO2>
A;Residues: 1-328,'SKECPSHIA' <TO2>
A;Cross-references: UNIPARC:UPI0000003FD2; EMBL:Y07519; NID:g55517; PIDN:CAA68812.1;
A;Note: it is uncertain whether Met-1, Met-7 or Met-19 is the initiator
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tominaga, S.I.
PEBS Lett. 258, 301-304, 1989
A;Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells
A;Reference number: S07054; MUID:90092495; PMID:2532153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Nucleotide sequence and functions of the oriT operon A;Reference number: A38529; MUID:91177811; PMID:1848841 A;Accession: B38529
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A; Residues: 1-191,'V',193-328,'SKECPSHIA' <TOM>
A; Residues: 1-191,'V',193-328,'SKECPSHIA' <TOM>
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                                                                                                                                                                      A; Genome: plasmid C; Superfamily: Es
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-899 < FUR>
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F;60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn)
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Best Local
                                                   Query Match
     Local Similarity
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Pred. No. 1.3;
20; Mismatches
Score 83; pred. No.
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                                             Length
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F;25-607/Product: 74K Serum attumin From Your SAl>
F;22-201/Domain: serum albumin repeat homology <SAl>
F;22-201/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;30/Binding site: copper (His) #status predicted
F;30/Binding site: copper (His) #status predicted
F;80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,4
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Dates: Silver, Solosia; Roscala #sequence from the complementary deoxyribalistic from the complementary deoxyri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 459-502,'t,'504-557 <WOL>
A;Cross-references: UNIPARC:UPI000017441F; GB:M28276
A;Cross-references: UNIPARC:UPI000017441F; GB:M28276
A;Note: the authors translated the codon TAT for residue 63 as
C;Comment: Serum albumin is synthesized in the liver as preproa
mones (weak bonds with these hormones promote their transfer ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI000017441E; EMBL:Z26826 R;Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, Eur. J. Biochem. 146, 489-496, 1985 A;Title: Deinduction of transcription of Xenopus 74-kDa A;Reference number: A05288; MUID:85126974; PMID:3971963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P14872; UNIPARC:UPI00001714FB; R;Schorpp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U. J. Mol. Biol. 199, 83-93, 1988
A;Title: 5'-flanking and 5'-proximal exon regions of the twagner. S02692; MUID:88172470; PMID:2451026
                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;19-24/Domain: propeptide #status predicted <PRO>F;25-607/Product: 74K serum albumin #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: carrier protein; duplication; glycoprotein; F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-48 < SCH >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S02693
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A;Accession: B41682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A05288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 3-607 < MOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: serum albumin, serum albumin repeat homology metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            during development.
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 QIYDSVRHTLKSLGLADHQYVSA-VHTDTDN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                    44 DIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSAN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 LKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL---TCP-----SCDSYEKKPPK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                          EINDFAKSCINDKTPECEKPVGTLFFDKLCADPAVGVNYEWSKECCAKQDPERAQCFKAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFLERFKSLLQKM---IHQHLSSRTHGSEDS
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                       Score 82; DB
Pred. No. 11;
19; Mismatches
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                                                                                                                                                                                                                                                                                     ; DB 1;
. 11;
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                                                                                                                                                                                                                                                                                                                  Length 607
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-PPSTNAGRRQKHRLTCPS 124
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                                                                                                                                                                                                                                           Gaps
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                                                                                      131
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C;Species: Azotobacter vinelandii
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C;Accession: JC7822; PC7187
R;Sahara, T:; Takada, Y:; Takeuchi, Y:; Yamaoka, N:; Fukunaga, N.
Biosci. Biotechnol. Biochem. 66, 489-500, 2002
A;Title: Cloning, sequencing, and expression of a gene encoding the monomeric A;Reference number: JC7822; PMID:12005040; MUID:2199801
A;Accession: JC7822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YIL127c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YI8277.02c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S49882
R;Hamlyn, N.; Churcher, C.
R;Hamlyn, N.; Churcher, C.
                                                                                                                                                                                                                                                        A;RESIQUES: 2-10 COLLIPARC:UPI000017CDF5
A;Cross-references: UPIPARC:UPI000017CDF5
C;Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate C;Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate C;- Language is twoical mosophilic, it contributes to the respiratory protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
JC7822
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A;Cross-references: A;Map position: 9L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isocitrate dehydrogenase (NADP) (EC 1.1.1.42), monomeric type - Azotobacter vinelandii
                                                                                                                Query Match
Best Local
                                                                                                                                                                                                             Superfamily: isocitrate dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                Similarity
                                              DRHMIRMRQLIDIVDQLKNYVNDL-----VPEFLPAPEDVETNCEWSAFSCFQKAQLKS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSED 161
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  DANIIKLPNISASVPQLKAAIKELQQQGYKLPDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLVKKKKVKKHKL--------DKEQLEQLAKHQVLKK--HQHEGTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEEEDKE--KCFSEKMKQLMK-----QSHSIED
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ilarity 24.8%;
Conservative 2
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                                                                                            23;
                                                                                       Score 78; DB Pred. No. 31; Pred. No. 31; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB :
Pred. No. 6.4;
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                                                                                                                                                                                                               monomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                      2; Length 741,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
                                                                                            34;
                                                                                                                                                                                                             type
  PEEPKTDTEKDVKARYDKIKGSA 133
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                                                                                            Indels
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C;Species: Saccharomyces cerevisiae
G;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #t(C;Accession: S60441; S64459
R;Skala, J; Nawrocki, A.; Goffeau, A.
Yeast 11, 1421-1427, 1995
A;Title: The semianna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P06607; UNIPARC:UPI0000080099; GB:X04754; NID:g8844; R;Garabedian, M.J.; Shirras, A.D.; Bownes, M.; Wensink, P.C. Gene 55, 1-8, 1987
A;Fitle: The nucleotide sequence of the gene coding for Drosophila melanogaster y A;Reference number: A27388; MUID:87305580; PMID:3114046
A;Cross-references: UNIPROT:P48237; UNIPARC:UPI000005309F; I R;Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; submitted to the Protein Sequence Database, May 1996
A;Reference number: S64428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 15, 67-85, 1987
A;Title: Sequence homologies among the three yolk polypeptide
A;Reference number: A25876; MUID:87146365; PMID:3029679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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C;Keywords: egg yolk; glycoprotein; phosphoprotein; sulfoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A27388; A; Accession: A27388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: FlyBase:Yp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-420 <GAR>
A;Cross-references: UNII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-420 <G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names:
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                                                                                    A;Molecule type: DNA
A;Residues: 1-864 <SKA>
                                                                                                                              A;Status: nucleic acid sequence not shown
                                                                                                                                                       A; Accession:
                                                                                                                                                                        A;Reference number: S60435; MUID:96158062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-420 <YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A25876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        itellogenin III precursor - fruit fly (Drosophila melanogaster)
;Alternate names: yolk polypeptide ypIII; yolk protein 3
;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Accession: A25876; A27388
;Yan, Y.L.; Kunert, C.J.; Postlethwait,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Date: 04-Mar-1988 #sequence_revision 12-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 QPGFGEDEVTIVLTGLPKTSPAQQKAMRRLIQAYVQKYNL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VNPVLREGNSDRRAPLSVKNYARKHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                       S60441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -HDLTPSFVPSPSNVPV---WIIKSNGQKVECKLNNYVETAKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76.5;
Pred. No. 2
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                                                                                                                                                                           PMID:8585325
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                                                                                                                                                                                                                                                                                                   #text_change 09-Jul-2004
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                                                EMBL:X85807; NID:g1045249; Talla, E.; Nawrocki, A.;
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ureidoglycolate hydrolase (EC 3.5.3.19) - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YIR032c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Pate: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 05-Oct-2004
C;Accession: S42022; S48494
R;Yoo, H.S.; Cooper, T.G.
Yeast 7, 693-698, 1991
A;Fitle: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A;Fitle: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A;Fitle: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A;Fitle: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A;Fitle: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.
A;Footecide ureidoglycoll
                                                                                                                                                                                                                                                                                                                                  A;Cross-retering
C;Genetics:
C;Genetics:
A;Gene SGD:DAL3
A;Cross-references: SGD:S0001471; MIPS:YIR032c
A;Map position: 9R
C;Superfamily: ureidoglycolate hydrolase; lipoprotein; methylated carboxyl end; E;192/Binding site: farnesyl (Cys) (covalent) #status predicted
F;192/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status prediction; hydrolase; lipoprotein; methylated carboxyl end; F;192/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status prediction; hydrolase; lipoprotein; methylated carboxyl end; F;192/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status prediction; hydrolase; lipoprotein; methylated carboxyl end; F;192/Modified site: methylated hydrolase; lipoprotein; methylated hydrolase; lipoprotein; methylated carboxyl end; F;192/Modified site: methylated hydrolase; lipoprotein; lipoprotein; lipoprotein; lipoprotein; lipo
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A;Residues: 1-864 <VAN>
A;Cross-references: UNIPARC:UPI000005309F; EMBL:Z72935; NID:gl323253; PIDN:CAA97164.1;
A;Experimental source: strain S288C
C;Genetics:
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Best Local Similarity
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                                                 73
                                                                                                                                   84 LKSANTGNNERIINVSIKKLKRKPPST 110
                                                                                                                                                                                                                                                                                                           24 VHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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                                                 LNRVFTQGSNQAISHSIKVLEKHPCST
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Pred. No. 49;
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A;ACCESSACH.
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-336 <BER>
A;Residues: 1-336 <BER>
A;Cross-references: UNIPROT:Q62611; UNIPARC:UPI000002AC15; GB:U04319; NID:g488278; PIDN:I
A;Cross-references: UNIPROT:Q62611; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-406 <ADAV>
A;Cross-references: UNIPROT:Q22975; UNIPARC:UPI000007865A; EMBL:U64845; PIDN:AAC48032.1;
A;Experimental source: strain Bristol N2; clone F45F2
A;Experimental source: strain Bristol N2; clone F45F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F45F2.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fit-18 protein precursor - rat (;Species: Rattus norvegicus (Norway rat) C;Decies: Rattus norvegicus (Norway rat) C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: S42632
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: A; Introns: 1/2;
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A; Accession: T28957
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R;Davidson, S.; Wohldmann,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:F45F2.11
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                                                VSFNAFDEVKRAAQAKTAKSPSTSSLERRAQRF-CPA-DFQPLPPPHIYIEMIRTLAP--
                                                                                           IINVSIKKLKR-----KPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKM 147
                                                                                                                                                ENEEKCEFRPVVTPNEIDSHKEWYHRLLMLKLEYKRGERGAFPPFPPPPPPLPSMMIAASNA 126
                                                                                                                                                                                                -----APEDVETNCEW---
                                                                                                                                                                                                                                                 KSSPQSSDENFFKRLQWGKIRLELK-----TPEFLKESSELEIEKNEKSGIQKCGENEG
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20.5%; Pred. No. 28;
ative 23; Mismatches
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22.2%; Pred. No. 23;
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R;Jackson-Grusby, L.; Kuo, A.; Leder, P. Genes Dev. 6, 29-37, 1992
Genes Dev. 6, 29-37, 1992
A;Title: A variant limb deformity transcript expressed in the embryonic mouse limb A;Reference number: S24407; MUID:92112033; PMID:1339380
A;Accession: S24407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKFZp434C0816.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46352
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A; Accession: T46352
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A; Residues: 1-1206 < JAC>
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C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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311
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37; Conser
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                                  SED
                                                                                                                                                                                                        LHSEDTLOMDGHILDSKRYAVIGADLRDLSELEEKLKKCNMNTQLPTLLIAECVLVYMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYVVKYYLRYYDQEAGTDKSVFPLPEPQDFFLASQVKFEDLLK-DLRKLKRQLEAS---- 1067
GNE 313
                                                                                                   QKHRL----TCPSCDSYE--KKPPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RASKGLLHMKSVKDILALILAFGNYMNGGNRTRGQADGYSLEILPKLKDVKSRDNGMNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSSPG--NMERI--VICLMVIFLGTLVHKSSSQGQ-DRHMIRMRQLIDIVDQLKNYVN--
                                                                  QKERLLSNGWETASAVDMMELYNRLPRAEVSRIESLEFLDEMELLEQLMRHYCLCWATKG
                                                                                                                                     EQSANLLKWAANS-FERAMFINYEQVNMG--DRFGQIMIENLRRQCDLAGVETCKSLES
                                                                                                                                                                    EDVETNCEWSAFSCFOKAQL---KSANTGNNERIINVSIKKLKRKP-----PSTNAGRR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROKHRLTCPSCDSYEKKPPKEFLERFKSLLOKMIHOHLSSRTHGSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGR
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                                                                                                                                                                                                                                                                            Conservative
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                                  161
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                                                                                                                                                                                                                                                                                              8.8%;
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22.0%; Pred. No. 8
                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                           Score 75; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 86;
l; Mismatches
                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                   -EFLERFKSLLQKMIHQHLSSRTHG 158
                                                                                                                                                                                                                                                                            64;
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                                                                                                                                                                                                                                                                                                           Length 321
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RESULT 15
S41211
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A;Accession: F82881
A;Sreture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <GLA>
A;Cross-references: UNIPARC:UPI00000ClC9A;
A;Experimental source: serovar 3; biovar 1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004 C;Accession: S41211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision
C;Accession: F82881
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A;Residues: 1-482 <COL>
A;Cross-references: UNIPROT:P54284; UNIPARC:UPI0000160BD2; GB:L27584; NID:g443663; PIDN:
C;Superfamily: human voltage-dependent calcium channel beta chain
                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 220, 257-262, 1994
A;Title: Cloning, chromosomal location and functional expression
A;Reference number: S41211; MUID:94164167; PMID:8119293
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                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S41211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            voltage-dependent calcium channel protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: UU505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein UU505 [imported] - Ureaplasma urealyticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Accession: S41211
;Collin, T.; Lory, P.;
                                                                                                                                                                                                       Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 KPIINVKNVDDKNKQENSTKLKNNDFISNNDKNNK--INENNNISYEEKPFK--LKRFNI 182
                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLK------NYVN----DLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNN
                                                                                           PAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHR-- 119
                                                                                                                                EAFAVRTNVSYCGVLDEECPVQGSGVN-FEAKDFLHIKEKYSNDWWIGRLVKEGGDIAFI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          r----rokminohrssrthgseds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGIISLLIVITAIILGVILSTQNTNKISKKEPLTQIEDNINNKKQDAH--KVNENITIID
                                                                                                                                                                 ERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKN--YVNDLVPE----FL
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                                                        PSPORLE-----SIRLKOEQKARRSGNPSSLSDIG---NRRSPPPSLAKOKOKOAEH 166
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taviaux, S.;
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-LTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHG 158
                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                       Score 74.5; D
Pred. No. 41;
27; Mismatches
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.; Berta, P.; Nargeot,
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Db 167 VPPYDVVPSMRPVVLVGPSLKGYE------VTDMMQKALFDFLKHRFDG 209
Search completed: September 7, 2006, 12:52:26
Job time : 14.8029 secs

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Result
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Gapop 10.0 , Gapext 0.5
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IL21 BOVIN
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IL21 CANFA
IL21 CONFA
IL21 MOUSE
QSSUB2 MOUSE
IL21 PERMA
QSBIG CHICK
Q3BIG TETMG
IL15 FELCA
Q6FGX7 HUMAN
IL15 HUMAN
IL15 HUMAN
IL15 HUMAN
032PM5_BRARE
II15_CERAE
II15_MCRUU
Q4U0U2_MACTH
Q2PUG6_RABIT
Q5D095_MOUSE
ILR11 MOUSE
ILR11 MOUSE
ILR15_SHEEP
Q75SZ9_CAVPO
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Q5EEK6_MARMO
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RE NUCLEOTIDE SEQUEN RX MEDLINE=22388257; RA Strausberg R.L., RA Klausner R.D., Co RA Altschul S.F., Ze RA Hopkins R.F., Jor RA Diatchenko L., Ma RA Brownstein M.J., RA Brownstein M.J., RA Raha S.S., Loquel RA Richards S., Worl RA Richards S., Worl RA Villalon D.K., Ma RA Fahey J., Helton RA Whiting M., Madan RA Blakesley R.W., T RA Rodriguez A.C., G RA Rodriguez A.C.,	ha ha lCR	CLEOT Tall Tall Tall Tall Tall Tall Tall Ta	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	32 33 34 35 35 36 37 38 30 30 30 30 30 30 30 41 41 42 41 42 41 42 43 43 43 43 44 43 43 43 44 43 44 43 44 44
CE Pu Pei Pi	EQUENCE (GENOMIC Braun A.C., Wont Livingston R.J., Livingston R.J., S.S., Sherwood J.K. HLBI HL66682 p 1e, WA (URL: http EP-2004) to the E	PubMed=110815 Dillon S.R., Dillon S.R., ton J., Madden tel M., Brandt tell S.R., Berr tell S.R., Berr A., Yao L., S.nsky K., Holly nd its recepto phocyte functi 2000).	STANDARD; integrated into sequence version 24 1 precursor (IL- 1 (Human) (Human) tazoa; Chordata; heria; Euarchont	10.1 105 2 Q5W 10.1 162 2 Q5W 10.1 162 2 Q5W 10.1 278 2 Q4Z 10.0 311 2 Q8D 9.9 511 2 Q5W 9.9 722 2 Q8D 9.9 1516 2 Q4W 9.8 582 2 Q8D 9.8 414 2 Q7M 9.8 607 2 Q4E 9.8 899 2 Q5Z 9.8 899 2 Q5Z
MRNA). by DOI-10.1073/pnas rouse L.H., Derge J rer L., Sheamen C.M. wax S.I., Wang J. wax S.I., Wang J. wax S.I., Wang J. cr A.A., Rubin G.M. flo M.F., Casavant T.I s G.J., Abramson R.I s G.J., Malek J.A., (a) Garcia A.M., Gay J gren E.J., Lu X., Gil Madan A., Rodrigues Shevchenko Y., Bout ceen E.D., Dickson M mutz J., Myers R.M.,	, Chung M .L., Robert ak L.A., Ni for genoming gs.washingi	JULAR LOCATION 1=10.1038/3504 1 A., Hammond A (u W., West J., injper J.L., Kr. Shiota J.L., Bor J., Lofton-Da J., Webster P., Foster D.; involved in NK	T; 155 AA. ProtKB/Swiss-Prot. (Zall). (zall). ires; Vertebrata;	QSW7F6 BRARE Q4GZL1_BUBBU Q5WQVB_MARMO Q4Z302_PLABE Q81913_LOXLA Q5AZU1_CANAL Q8AZU1_CANAL Q8DGP4_VIBVU Q4WQU6_ASPFU Q8DU36_SYNEL Q82933_9POTV Q7MNL4_VIBVY Q641P7_XENLA Q4F1J3_SENTR Q52336_9ZZZZ ALIGNMENTS
J.G., Candler G.D., Schuler G.D., Schuler G.D., Bhat N.K., Hong L., Scheetz T.E., Prange C., D., Mullahy S.J., Gunaratne P.H., Gunaratne P.H., L.J., Hulyk S.W., Lbb R.A., Lbb R.A., Liffard G.G., A.C., G.G.,	-W., Nguyen C.P., Leon P.D., ickerson D.A.; capplications, UW- con.edu).";	, AND TISSUE 5504; Sprecher C., Schrader S., amer J., t S., Hambly K., y C., Gilbert T., Whitmore T., whitmore T.,	Euteleostomi; rrhini; Hominidae;	QSw7f6 brachydanio Q4gz11 bubalus bub Q5wqv8 marmota mon Q4z302 plasmodium Q8i913 loxosceles Q5a2ul candida alb Q8d6p4 vibrio vuln Q4wqu6 aspergillus Q8djs6 synechococc Q8293 johnsongras Q7mn14 vibrio vuln Q44fij salmonella Q52336 plasmid r64

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REVIEW
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                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSG00000138684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3L; AF254069; AAG29348.1; ALT_INIT; mRNA.
1L; AY763518; AAU88182.1; ALT_INIT; Genomic_DNA.
3L; BC066258; AAH66258.1; ALT_INIT; mRNA.
3L; BC066259; AAH66259.1; ALT_INIT; mRNA.
3L; BC066260; AAH66260.1; ALT_INIT; mRNA.
1L; BC066261; AAH66261.1; ALT_INIT; mRNA.
3L; BC066261; AAH66262.1; ALT_INIT; mRNA.
3L; BC066262; AAH66262.1; ALT_INIT; mRNA.
3L; BC069124; AAH69124.1; ALT_INIT; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 605384; gene.
GO:0005615; C:extracellular space; NAS.
GO:0005134; F:interleukin-2 receptor binding; IPI.
GO:0048469; P:cell maturation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells (By similarity). May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells. During T-cell mediated immune response may inhibit dendricic cells (DC) activation and maturation.
                                                                                                                                                                                                                                                                                                                                                                                            GO:0042102; P:positiv
GO:0007165; P:signal
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TISSUE SPECIFICITY: Expressed in activated
                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0045078;
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                                                                                                                                                                           Similarity
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                                                                                            MERIVICLMVIFLGTLVHKSSSQGODRHMIRMRQLIDIVDQLKNYVNDLVPEFLFAPEDV
                                                                                                                                                                                                                                                                                                                                 ; Glycoprotein; 9
1 22
23 155
                    ETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDS
                                                                           MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV
ETNCEWSAFSCFQKAQLKSANTGNNER I I NVS I KKLKRKPPSTNAGRRQKHRLTCPSCDS
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        P:positive regulation of interferon-gamma bio. P:positive regulation of T cell proliferation; P:signal transduction; NAS.
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17923
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N-linked TGlcNAc. . .) (Po Potential.
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Pred. No. 1.8e-64;
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Mammalia; Eutheria;
Pecora; Bovidae; Bov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12969638; DOI=10.1016/S0165-2427(03)00106-5; Muneta Y., Kikuma R., Yoshihara K., Mori Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q76LŪS;
                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning,
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                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted progressed in heart, kidney, liver, and lung
                                                                                                                                                                                                                                                                                                                                                               . Immunol. Immunopathol. 95:73-80(2003).

FUNCTION: Cytokine with immunoregulatory activity. May promote transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and cells in response to activating stimuli. In synergy with IL15 title stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response inhibit dendritic cells (DC) activation and maturation (By
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           YEKKPPKEFLERFKSLLQKMIHQHLS
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                                                                                                                                 Score 629; DB 1;
Pred. No. 4.4e-48;
2; Mismatches 15
                                                                                                                                                                                       Potential
                                                                                                                                                                                                   Potential
                                                                                                                                                                                                                        Interleukin-21
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                                                                                                                                                                             696566DA73F4B8BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            distribution
                                                                                                                                                                                                                                                                                                                                             protein.
                     153
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                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                                                   spleen,
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Best Local
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DISULFID
SEQUENCE
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                          Q6L7I9;
23-NOV-2004,
                                                     05-JUL-2004,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND SUBCELLULAR LOCATION PubMed=15107555; DOI=10.1292/jyms.66.269; Muneta Y., Kikuma R., Uenishi H., Hoshino T., Yoshihara K., Ta Hamashima N., Mori Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-2004, sequence version 07-FEB-2006, entry version 12. Interleukin-21 precursor (IL-2
                            Name=IL21;
                                       Interleukin-21 precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin-21.",
J. Vet. Med. Sci. 66:269-275(2004).
-!- FUNCTION: Cytokine with immunor
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                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted protein. SIMILARITY: Belongs to the IL-21 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation.
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                                                                                                                                                                                                                                                                   MEKTVICLMVIFSGTVAHKSSFQGQDRLLIRLRQLIDTVDQLKNYVHDLDPELLPAPEDV
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                                                    sequence version entry version 11.
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71
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118
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Potential.
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Pred. No. 2.
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Q9ESIT;
23-NOV-2004,
01-MAR-2001,
07-FEB-2006,
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DISULFID
SEQUENCE
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogn
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20531754; PubMed=11081504; DOI=10.108/35040504; Parrish-Novak J. Dillon S.R., Welson M., Hammond A., Spreche Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J.,
                                         STRAIN=BALB/c
                                                 NUCLEOTIDE SEQUENCE [MRNA].
                                                                   NCBI_TaxID=10090;
                                                                                                             Mus musculus (Mouse)
                                                                                                                     Name=Il21
                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9615;
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                                                                                                                             Interleukin-21 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl;
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71
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118
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canine interleukin-21 cDNA."
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                                                                                                                                                                                                                                                                                                                                                                                             MW;
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Pred. No. 7.4e-46;
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           Sprecher C.
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Brandt K., Bulfone-Paus S., Foster D.C., Rueckert R.;
"Interleukin-21 inhibits dendritic cell activation and
Blood 102:4090-4098(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasaian M.T., Whitters M.J., Carter L.L., Lowe L.D., Jussif J. Deng B., Johnson K.A., Witek J.S., Senices M., Konz R.F., Wurster A.L., Donaldson D.D., Collins M., Young D.A., Grusby N"IL-21 limits NK cell responses and promotes antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamb Mudri S., Clegg C., Moore M., Grant F., J., Lofton-Day C., Gilb. Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore Maurer M., Kaushansky K., Holly R.D., Foster D., "Interleukin 21 and its receptor are involved in NK cell exparegulation of lymphocyte function."; Nature 408:57-63(2000).
                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B cells."
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Delwail A.,
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                                                                                                                                                            Cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunity 16:559-569(2002).
                                                                                                                                                                                                                                                                                                                                                FUNCTION: Cytokine with immunoregulatory activity. May promote transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with ILIS. May regulate proliferation of mature B- and cells in response to activating stimuli. In synergy with ILIS timulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response inhibit dendritic cells (DC) activation and maturation. SUBCELLULAR LOCATION: Secreted protein.
                                                                                                                                                                  L; AF254070; AAG29349.1; -; mRNA.
L; AY428162; AAR06254.1; -; mRNA.
L; AY428162; AAR06254.1; -; mRNA.
embl; ENSMUSG00000027718; Mus musculus.
GO:0005615; C:extracellular space; TAS.
GO:0005126; F:hematopoletin/interferon-class (D200-domain. GO:0045579; P:positive regulation of B cell differentiation GO:001783; P:programmed cell death, B cells; NAS.
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             Similarity
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A., Foster D., Lecron
s a switch factor for
                                                                                                                                                           Glycoprotein;
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             57.2%;
63.0%;
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23;
Score 486; DB
Pred. No. 2.5e
23; Mismatches
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n J.C., Yssel H.;
r the production (
                                                     Potential.
D2527ED95BA15194 CRC64;
                                                                                  Interleukin-21.
/FTId=PRO_0000015506.
N-linked (GlcNAc. . .) (Potential).
Potential.
                                                                                                                                                Potential
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ve the a
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anti-tumor effect
             DB 1;
.5e-35;
                                                                                                                                                                        cell differentiation; NAS cells; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guglielmi
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                           Length 146;
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tigen-specific T ce
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Best Local 9
                                                                                                                                                                    Peromyscus maniculatus (Deer mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
Muroidea; Cricetidae; Neotominae; Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=I121; ORFNames=DN-452A22.7-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2005, integrated into 1 10-MAY-2005, sequence version 07-FEB-2006, entry version 3. Interleukin 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSSUE2 MOUSE
QSSUE2;
                                                                                                                                                                 Name=Il21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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NUCLEOTIDE SEQUENCE
                                       NCBI_TaxID=10042;
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bl; ENSMUSG00000027718; Mus musculus.
bl; ENSMUSG00000017718; Mus musculus.
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  [MRNA]
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Pred. No. 2.5e-35;
3; Mismatches 31;
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                                                                                             Rodentia; Sciurognathi;
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RESULT Q581U67 ID 8106 ID 910 205 PM 266 PM 
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Q58IU6_CHICK
Q58IU6;
26-APR-2005,
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NON_TER
SEQUENCE
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DISULFID
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"Cloning
cDNAs.";
EMBL; AY943833;
SEQUENCE 145 /
                                                                                                                                               Shao J., Dong W., Xiang L.; Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                         Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                        Interleukin 21.
                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-2005, sequence version 07-FEB-2006, entry version 4.
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                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                    Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Secreted protein (By similarity)
SIMILARITY: Belongs to the IL-21 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.FACFQKAKLKPANTGSNKTIISDLVTQLRRRLPATKAEKKQQSLVKCPSCDSYEKKTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 MVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
  145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       integrated into UniProtKB/TrEMBL
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56
63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
  AAX40651.1; -
AA; 16637 MW;
                                                                                                                                                                                                                                                                                                    Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
107
110
                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.1%;
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                       .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 392; DB 1;
Pred. No. 5.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-21.
/FTIG=PRO 0000015507.
N-linked (GlCNAc. . .) (Potential).
Potential.
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  mRNA.
E70AB6A568CDABE6
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                                                                         see http://www.uniprot.org/terms
Attribution-NoDerivs License
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  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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AC 097687
AT 01-MAY
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DE Interl
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.Matches
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Best Local Similarity
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22-NOV-2005, sec
07-FEB-2006, ent
Interleukin 21
                                                                             30-MAY-2000, integrated into UniProtKB/Swiss-Prot 01-MAY-1999, sequence version 1. 07-FBB-2006, entry version 23. Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Head kidney;
Wang H., Shao J., Xiang L., Dong W.;
Wang H., Shao J., Xiang L., Dong W.;
"Molecular cloning and expression analysis of an IL-21 homolog
Tetraodon nigroviridis.";
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                    097687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q38121_TETNG
Q38121;
  Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      GRROKHRLTCPSCDSYEKKPPKEFLERFKSLLOKMIHQHLSS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VETNCEWSAFSCF-----QKAQLKSANTGNNERIINVSIKKLKRKPPSTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKQLVFCLFAVCCWWLADASSAECSERKLEEVRRELEGVNNTLQN--RELL--LTTPPKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERIVICLMVIFLGTLVHKSSSGGGDRHMIRMRQLIDIVDQ-LKNYVNDLVPEFLPAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CESYERKKPQEFLNSFSKLMQKLFKNSTAER 139
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                                                                                                                                                                                                                                                                                                                                         -----TCQTCNSHPQEKVGEFFSRLDSFIQKAISKLRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                         IEEGCCLSALRCFRDSIQENIKSTVRLQRRLYKSLNNSHTAACLNFC---
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25.3%;
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Pred. No. 2.9e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 119.5; DB Pred. No. 0.013; 9; Mismatches
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Best
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Q6FGX7;
10-MAY-2005,
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CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF108148; AAD05268.1; -; mRNA.
                                                                                                                                                                         10-MAY-2005, sequence version 07-FEB-2006, entry version 6. IL15 protein (Interleukin 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                        Halleck A., Ebert L., Mkoundinya
Neubert P., Kstrang K., Schart J.
Korn B., Zuo D., Hu Y., LaBaer J.
Submitted (JUN-2004) to the EMBL/
                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                Name=IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003443; Interleukin 15.
PANTHER; PTHR11323; Interleukin 15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Euthe
Felinae; Felis
                                                                                                NCBI_TaxID=9606;
                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02372; IL15; 1.
Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9685;
 NUCLEOTIDE SEQUENCE
                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                CLMVIFLGTL---VHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETN
                                                                                                                                                                                                                                                                                                       ECEELEEKNIKEFLOSFVHIVOMFIN 160
                                                                                                                                                                                                                                                                                                                             SCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                      CKVTAMKCFLLELHVISLESKNETIHQTVENIII-----LANSGLSSNRNITETGCK 134
                                                                                                                                                                                                                                                                                                                                                                              CEWSAFSCF----QKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLT----CP
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127
83
90
162 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                  integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                  .
Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106.5; DB Pred. No. 0.21; 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
/FTId=PRO 0000015395.
InterleukIn-15.
/FTId=PRO 0000015396.
N-linked (GlcNAC. . .) (N-linked (GlcNAC. . .)
                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
DBC7CEF7F40110DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
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                                                                                                                                                                            isoform
                                                                                                                                                                                                                                         PRT;
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: :
                                                 Schick M., Eise
Shen B., Henze
                                                                                                                                                                                                                                         135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                              Eisenstein
                                                                                                                             Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
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                                                                                                                                                                                                                                                                                                                                                                              123
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RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Schein J.E., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
RT S. Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC100962; AAI00963.1; -; mRNA.
EMBL; CR542007; CAG46604.1; -; mRNA.
EMBL; CR542007; CAG46604.1; -; mRNA.
EMBL; CR541980; CAG46777.1; -; mRNA.
EMBL; BC100961; AAI00962.1; -; mRNA.
EnsembL; ENG600000164136; Homo sapiens.
EnsembL; ENG600000164136; Titerfeutin/interferon-class (D: GO; GO:0006955; P:immune response; IEA.
InterPro; ITR003443; Interleukin_15.
PANTHER; PHR11123; Interleukin_15; 1.
                                                   IL15_HUMAN STANDARD; PRT; 162 AA.
P40933; O000440; O43512; Q93058; Q9UBA3; .
01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
01-FEB-1995, sequence version 1.
07-FEB-2006, entry version 43.
Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                     HUMAN
                                       Name=IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=PCR/rescued clones;
Bukaryota;
                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF02372; 141.
NCE 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                       94 RIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDSYEKKPPKEFLERFKSLLOKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project;
                                                                                                                                                                                                                                                                                                                                                                                   VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD
                                                                                                                                                                                                                                                                                         TVENLII--LANNSLSSNGNVTES---GCKECEELEEKNIKEFLQSFVHIVOMFIN
                                                                                                                                                                                                                                                                                                                                                                                                                             IDIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rescued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14912 MW; EB44F422096B143E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99.5; D
Pred. No. 0.72
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (D200-domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stemstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stemstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne-P.H.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Rahey J., Helton E., Ketteman M., Madan A., Gabis R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

A Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grabstein K.H., Bisenman J., Shanebeck K., Rauch C., Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A., Ahdieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M., Giri J.G.; "Cloning of a T cell growth factor that interacts with the beta chain of the interleukin-2 receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               through alternate usage of signal peptides.";
Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meazza R., Verdiani S., Biassoni R., Coppolecchia M., Gaggero A., Orengo A.M., Colombo M.P., Azzarone B., Ferrini S.; "Identification of a novel interleukin-15 (IL-15) transcript isoform
                        TISSUE=Epidermis;
Sorel M.A., Jacques Y.;
"IL15 expression in hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM IL15-S48AA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression of two IL-15 mRNA isoforms in human tumors does correlate with secretion: role of different signal peptides. Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meazza R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bamford R.N., Waldmann T.A.; "Generation of secretable interleukin 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tagaya Y., Kurys G., Thies T.A.,
Bamford R.N., Waldmann T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98070771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 12:2187-2192(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96218668; PubMed=8668345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA)
Krause H., Jandrig B., Wernicke C., Bulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 264:965-968(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=94233380; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SEP-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jandrig B.,
                                                                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9405632; DOI=10.1073/pnas.94.26.14444;
G., Thies T.A., Losi J.M., Azimi N., Hanover J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8178155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
human keratinocytes.";
) to the EMBL/GenBank/DDBJ databases.
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                                                                                          49-162
                                                                                                                                     U.S.A.
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                                                                                                                                   99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      small cell lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanover J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer cell
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Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                          HGNC; HGNC:5977; ILIS.

MIM; 600554; gene.

GO; GO:0005768; C:endosome; TAS.

GO; GO:0005761; C:extracellular space; TAS.

GO; GO:0005794; C:GOlgi apparatus; TAS.

GO; GO:0005887; C:integral tro plasma membrane; TAS.

GO; GO:0005847; C:membrane fraction; TAS.

GO; GO:0005624; C:membrane fraction; TAS.

GO; GO:0005797; P:cell-cell signaling; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0006955; P:immune response; TAS.

GO; GO:0008284; P:positive regulation of cell pro

GO; GO:0007165; P:signal transduction; TAS.
                                                     CONFLICT
SEQUENCE
                                                                                                                                                                CARBOHYD
DISULFID
DISULFID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U14407; AAA21551.1; -; mRNA.
EMBL; Y91233; CAA62616.1; -; Genomic_DNA.
EMBL; Y94223; CAA63914.1; -; mRNA.
EMBL; X94223; CAA63913.1; -; mRNA.
EMBL; R031167; AAB97518.1; -; mRNA.
EMBL; Y09908; CAA71044.1; -; mRNA.
EMBL; BC018149; AAH18149.1; -; mRNA.
                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                      PANTHER; PTHR11323; Int
Pfam; PF02372; IL15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z38000; CAA86100.1;
Ensembl; ENSG00000164136;
                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                        Alternative splicing;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma but not In-ax alpus.
SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL1
secreted, but rather is stored intracellularly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the IL-15 family.

DATABASE: NAME=R&D Systems' cytokine source book: IL15;

WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=209".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Most abundant in placenta and It is also detected in the heart, lung, liver and $21AA is preferentially expressed in tissues such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Cytokine that stimulates the proliferation of T. lymphocytes. Stimulation by IL-15 requires interaction of with components of IL-2R, including IL-2R beta and probab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleus and cytoplasmic components. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=IL15-S21AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IL15-S48AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P40933-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P40933-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soId=P40933-3;
                                                     141
162
                                                                                                                                                                   127
83
90
                                                                                                             \vdash
                                                      À,
                                                      141
18086
                                                                                                                                                                   127
133
136
47
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                                                                                                             37
                                                                                                                                                                                                                                                                                                                   Interleukin_15;
                                                                                                                                                                                                                                                                            29
              11.7%;
                                                                                                                                                                                                                                                                                                                                Interleukin_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_002661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=VSP_002660;
                                                                                                                                                                                                                                                                                        Cytokine; Glycoprotein;
                                                        W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
              Score 99.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA.
                                                                    M
                                                                                       isoform 3).
/FTId=VSP 002661.
MRISKPHIRSISIOCYLCLLLNSHFLTEAGIHVFILG
                                                                  /FTId=VSP_002660
E -> K (in Ref.
                                                                                                                                                 MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSA
                                                                                                                                                                               Potentia
                                                                                                                                                                                             Potential
                                                                                                                                                                                                         /FTId=PRO_0000015394.
N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                     Interleukin-15
                                                                                                                                                                                                                                                                            Potentia
                                                                                                                                                                                                                                                 /FTId=PRO_0000015393
                                                      -> K (in Ref. 4)
0CE0520C1D8379E2
                           DB 1;
                                                                                                                                                                                                                                                                                        Signal
                                                                                                                                                                                                                                                                                                                                                             proliferation;
                                                         CRC64;
                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL15-S21AA is
                                                                                                                                                                                                          (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       appearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i skeletal
i kidney. I
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30;

Conservative

Mismatches 0.88;

48;

Indels

15;

Gaps

5

Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RC TISSUE=PCR rescued clones;

RX MEDLINE=2238357; pubMede12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=2238357; pubMede12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Heich F.,

RA Staustein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Scwanstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Gitmwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Gitmwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Gitmwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                        Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1928 HUMAN
Q49528 HUMAN PRELIMINARY, PR
Q49528,
Q49528,
13-SEP-2005, integrated into Uni
13-SEP-2005, sequence version 1
07-FEB-2006, entry version 2.
Interleukin 15, isoform 1.
                                                                                                                                                                                                                                                      EMBL; BC100963; AAI00964.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005126; F:hematopoietin/region-class (D200-domain.
GO; GO:0005955; P:immune response; IEA.
SEQUENCE 162 AA; 18086 MW; OCE0520C1D8379E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PCR rescued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
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                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project;
                                             RIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDSYEKKPPKEFLERFKSLLOKMIH
                                                                                        VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD
                                                                                                                                 IDIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVENLII--LANNSLSSNGNVTES---GCKECEELEEKNIKEFLQSFVHIVQMFIN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH
        TVENLII--LANNSLSSNGNVTES---GCKECEELEEKNIKEFLQSFVHIVQMFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acad. Sci.
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                              11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                        Score 99.5; DB 2;
Pred. No. 0.88;
23; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                   see http://www.uniprot.org/terms
Attribution-NoDerivs License
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                                                                                                                                                                            48;
                                                                                                                                                                                                               Length
                                                                                                                                                                            Indels
                                                                                                                                                                            15;
                                                                                                                                                                          Gaps
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RESULT 14
Q599U2_FUGRU
Q599U2_FUGRU
AC Q599U2_FUGRU
AC Q599U2_FUGRU
DT 26-APR-2005, s
DT 26-APR-2005, 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              TILIS_RABIT STANDARD; PRT; Q3Y5G8; O6-DEC-2005, integrated into UniPr 27-SEP-2005, sequence version 1. 07-MAR-2006, entry version 6. Interleukin-15 precursor (IL-15).
NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.

PubMed=15978671; DOI=10.1016/j.vetimm.2005.04.013;

Xiong C., Hixson P.M., Mendoza L.H., Smith C.W.;

"Cloning and expression of rabbit interleukin-15.";

vet. Immunol. Immunopathol. 107:131-141(2005).

vet. Immunol. Immunopathol. 107:131-141(2005).

vet. Troncorron: Cytokine that stimulates the proliferation of lymphocytes. Stimulation by IL-15 requires interaction of with components of IL-2R, including IL-2R beta and proba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15592926; DOI=10.1007/s00251-004-0741-7;
Bird S., Zou J., Kono T., Sakai M., Martinus Dijkstra J., Secombes C.
"Characterisation and expression analysis of interleukin 2 (IL-2) and
IL-21homologues in the Japanese pufferfish, Fugu rubripes, following
theirdiscovery by synteny.";
Immunogenetics 56:909-923(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, integrated into UniProtKB/TrEMBL 26-APR-2005, sequence version 1. 07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                            Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IL15;
                                                                                                                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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AJ584837; CAE50922.2; -; Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENIGDCCCLSALKCFRE-----NFKEIFSLTDLPQKKLYRSLTNTLTEKGLDFCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDVETNCEWSAFSCFQKAQLKSANTGNNERIINVS---IKKLKRKPPSTNAGRR----QK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQL---KNYVNDLVPEFLPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AA; 17777 MW; 61DEFE96BD52945E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98.5; DE
Pred. No. 1;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 155;
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Search completed: September 7, 2006, 12:51:29 Job time: 91.3314 secs
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InterPro; IPR003443; Interleukin_15.
PANTHER; PTHR11333; Interleukin_15; 1.
Pfam; PF02372; IL15; 1.
Cytokine; Glycoprotein; Signal.
SIGNAL 1 29
PROPEP 30 48 Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma but not IL-2R alpha (By similarity).
-!- SUBCELLULAR LOCATION: Secreted protein.
-!- TISSUE SPECIFICITY: Expressed in many tissues including heart, spleen, lung, liver, muscle and kidney (at mRNA level). Expressed in many tissues including heart, spleen, lung, liver, muscle and kidney (at protein level).
-!- SIMILARITY: Belongs to the IL-15 family.
                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                           111 VQNLIILANTSLSSKGNVTESG------CKECEELEEKNITEFLQSFIHIVQMFIN 160
                                                                            95 IINVSI---KKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                      52 DVISDLKR-IEDLIKSIHIDATLYTESDAHPNCKVTAMKCFLLELRVISHESRNMDINET 110
                                                                                                                                                     44 DIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNER 94
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18330 MW;
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N-linked (GlcNAc. ..)
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N-linked (GlcNAc. ..)
Potential.
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Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 12, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/Backfiles1.pep:*
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US-09-923-246-2
US-10-295-723-2
US-09-949-016-10307
US-10-282-622-4
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US-110-282-622-4
US-09-923-246-85
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US-09-923-246-73
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Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane V.
APPLICANT: Nelson, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LICETTER PREPERSOR.
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                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 2
LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-2
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US-09-522-217-2
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CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF 580 ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-189-193-3
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US-08-31-399-5
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120 120

60 60 Result No.

RESULT 2 US-09-923-246-2

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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/123,904
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PRIOR FILING DATE: FILING DATE: 1999-07-01
NUMBER OF SEO ID NOS: 115
SOPTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
GENERAL INFORMATION:
APPLICANT: No. 6686178AK, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Presher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Dillon, Stacey M.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723;
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2002-11-15
PRIOR FILING DATE: 2003-09
PRIOR APPLICATION NUMBER: US 60/123,547
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GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
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Patent No. 6686178
GENERAL INFORMATION:
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEO ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 162
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 162; Conserv
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APPLICANT: No. 677739ak, Julia
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
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PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
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APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
                                                                                                                                                                                                                                                                                                                           LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                      accn 100.0%; Score 850; DB 2; al Similarity 100.0%; Pred. No. 1.4e-86; 162; Conservative 0; Mismatches o.
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                                                                                                             61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
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                    TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                          LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERI INVSIKKLKRKPPSTNAGRRQKHRL
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100.0%; Pred. No. 1.4e-86;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-10307
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-2
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US-10-282-622-2
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Patent No. 681233
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS FILE REFERENCE: 01-37 CURRENT APPLICATION NUMBER: US/10/282,622 CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Presnell, Scott R. APPLICANT: West, James W. APPLICANT: No. 6929932ak, Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/337,586 PRIOR FILING DATE: 2001-11-05 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                            TYPE: PRT
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                                                                                                    Similarity
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MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
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No. 6929932ak, Julia E.
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                                                                                100.0%; Score 850; DB 2;
100.0%; Pred. No. 1.5e-86;
tive 0; Mismatches 0;
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; Sequence 6, Application US/10282; Patent No. 6929932; GENERAL INFORMATION: APPLICANT: Presenell, Scott R.; APPLICANT: West, James W.; APPLICANT: No. 69299328k, Juli
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US-10-282-622-6
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US-10-282-622-6
US-10-282-622-4
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Patent No. 6929932
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                  APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 69299328k, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
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APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
                                                                                                                                NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                  OTHER INFORMATION: zalphall ligand Q153ST/I156D
                                    FEATURE:
                                                    ORGANISM: Artificial Sequence
                                                                            TYPE: PRT
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98.1%;
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Pred. No. 1.8e-84;
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RESULT 10
US-09-923-246-85
(; Sequence 85, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FRANSEQ for Windows Version 3.0
SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Goss, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Nelson, Andrew J.

APPLICANT: Hammond, Angela K.

TITLE DEFERENCE: AGALG.

FILE DEFERENCE: AGALG.
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
-09-522-217-85
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 519
TYPE: PRT
                                                                                                                                                                     440
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                                                                                                                                                                                                                                                                                                                134;
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                                                                                                                     LLQKMIHQHLSSRTHGSEDS
                                                                                                                                                                   QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
                                                                                                                                                                                        QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS 142
                                                                                                                                                                                                                                          LVPRGS----QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCPSCDSYEKKPPKEFLERFKSLLQKM 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCPSCDSYEKKPPKEFLERFKSLLDKM
         Application US/09923246
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                                                                                                                                                                                                                                                                                                                             81.8%;
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98.6%;
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                                                                                                                                                                                                                                                                                                              Score 695.5; DB 2
Pred. No. 9.6e-69;
1; Mismatches 2
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Pred. No. 2.1e-76;
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                                                                                                                                                                                                                                                                                                                                              DB 2;
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FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

CURRENT FILING DATE: 2001-09-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FASCSEQ for Windows Version 3.0

SEQ ID NO 85
                                                      APPLICANT: Sprecher, Cindy A.
APPLICANT: Holty, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Nolson, Andrew J.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIFTLE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
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; OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-09-923-246-85
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APPLICANT: No. 66052772ak, Julia E
APPLICANT: Poster, Contt R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6686178
GENERAL INFORMATION:
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 85,
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APPLICANT:
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                  APPLICATION NUMBER: US 60/123,547 FILING DATE: 1999-03-09
APPLICATION NUMBER: US 60/123,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
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                                                                                                                                                                                                                                                                                                       Presnell, Scott R.
Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLOKMIHOHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | OLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10295723
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95.7%;
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Pred. No. 9.6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
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APPLICANT: Helson, Andrew J.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-01
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US-09-522-217-56
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US-09-522-217-56
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: No. 6307024ak, Julia E. APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Holly, Richard D. APPLICANT: Holly, Richard D. APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                   LENGTH: 146
                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 LLOKMIHOHLSSRTHGSEDS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                       92;
ETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLKSANTGNNER I INVS I KKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
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                                                                                                            MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLQKMIHQHLSSRTHGSEDS 519
                                                               MERTLYCLVVIFLGTVAHKSSPQGPDRLLIRLRHLIDIVEQLKIYENDLDPELLSAPQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09522217
                                                                                                                                                         Conservative
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                                                                                                                                                                            57.2%;
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95.7%;
                                                                                                                                                     ; Score 486; DB 2;
; Pred. No. 3.7e-46;
23; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 695.5; DB 2
Pred. No. 9.6e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: mus musculus US-09-923-246-56
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SEQ ID NO 56
LENGTH: 146
                                                                                                                                                                                             Sequence 56, Application US/10295723
Patent No. 6686178
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR APPLICATION DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEO ID NOS: 115
                                APPLICANT:
                                                                                  APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/923,246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
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Dillon, Stacey R.
Hammond, Angela K
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               Nelson, Andrew J.
Dillon, Stacey R.
Hammond, Angela K
                                                                    Johnston, Janet V.
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Pred. No. 3.7e-46;
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FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR PILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 56
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APPLICANT: Wo. 6777539ak, Julia E.

APPLICANT: West, James W.

APPLICANT: Presnell, Scott R.

APPLICANT: Presnell, Scott R.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: WOLSON, MARCH D.

APPLICANT: WOLSON, WO
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-09-825-561A-47
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US-09-825-561A-47
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; TYPE: PRT
; ORGANISM: mus musculus
US-10-295-723-56
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Best Local Similarity 63.0%;
Matches 92; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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Local Similarity 63.0%;
nes 92; Conservative 2
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                                                                                                              MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV 67
ETNCEWSAFSCFOKAOLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
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                                                                                                                                                                                                                                                                    ; Score 486; DB 2; Length 146; ; Pred. No. 3.7e-46; 23; Mismatches 31; Indels
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; Pred. No. 3.7e-46; 
23; Mismatches 31; Indels
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                                     128 YEKKPPKEFLERFKSLLQKMIHQHLS 153
                                                                           61 KGHCEHAAFACFQKAKLKPSNPGNNKTFIIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
YEKRTPKEFLERLKWILQKMIHQHLS 146
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Search completed: September Job time : 17.2 secs 7, 2006, 12:53:38

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006
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US-09-923-246-2
US-09-925-561A-10
US-09-927-218A-19
US-10-264-634-19
US-10-264-634-19
US-10-262-622-2
US-10-659-684-2
US-10-687-087-10
US-10-75-204-2177
US-11-174-398-2
US-10-174-398-2
US-11-174-398-6
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APPLICANT: Welson, Andrew J.
APPLICANT: Welson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
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; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Gross, Jane A.
; APPLICANT: Welson, Andrew J.
; APPLICANT: Nelson, Stacey R.
; APPLICANT: Dillon, Stacey R.
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-2
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Local Similarity 100.0%;
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                                                  TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
                           TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
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US-10-867-992-12
US-11-132-947-2
US-10-867-992-12
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US-10-867-992-10
US-11-132-947-12
US-10-867-992-4
US-10-867-992-6
US-10-867-992-6
US-10-867-992-2
US-10-867-992-2
US-10-867-992-2
US-10-867-992-2
US-10-867-992-2
US-10-868-56-298-4
US-10-872-888-56
US-10-295-723-56
US-10-659-688-56
US-10-659-688-56
US-10-872-087-47
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Pred. No. 2e-81;
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Result No.

Score

Query Match

162

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Gaps

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Minimum DB Maximum DB

length:

654321

Scoring table:

Title: Perfect score:

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

85, Appl 2, Appl 3, Appl 11, Appl 110, Appl 110, Appl 112, Appl 112, Appl 113, Appl 114, Appl 115, Appl 116, Appl 117, Appl 118, Appl 11

Sequence Sequence Sequence Sequence

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protein on

US-09-825-561A-10

Application US/09825561A

RESULT

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; SEQ ID NO 19
; LENGTH: 162
; TYPE: PAT
; TYPE: PAT
; ORGANISM: Human
; US-09-972-218A-19
                                                                                                               APPLICANT: Lowe, Leslie D.

APPLICANT: Unger, Michelle
TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
FILE REFERENCE: 22058-552CIP2
CURRENT APPLICATION NUMBER: US/09/972,218A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/569384
PRIOR APPLICATION NUMBER: 09/569384
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/560766
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/6057128
PRIOR APPLICATION NUMBER: US/6057128
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 21
SECOIT NOS: Patentin Ver. 2.1
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CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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Patent No. U
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APPLICANT: No. US20020137677Alak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAIL CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carter, Laura
APPLICANT: Whitters, Mai
APPLICANT: Collins, Mar
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TYPE: PRT
ORGANISM: Homo sapiens
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Collins, Mary
Young, Deborah A.
Donaldson, Debra D.
Lowe, Leslie D.
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; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
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PRIOR FILING DATE: 1998-03-17
PRIOR PELICATION NUMBER: 09/560,766
PRIOR FILING-DATE: 2000-04-28
PRIOR FILING-DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/569,384
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/972,218
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/373,746
PRIOR FILING DATE: 2002-04-17
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                                  Sequence 2, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, CAPPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/10264634 Publication No. US20030108549A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor FILE REFERENCE; GIS320-P3
CURRENT APPLICATION NUMBER: US/10/264,634
CURRENT FILING DATE: 2002-10-04
CURRENT FILING DATE: 2002-10-04
APPLICANT:
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Presnell, Scott R. Sprecher, Cindy A. Foster, Donald C. Holly, Richard D.
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100.0%; Pred. No. 2e-81;
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100.0%; Pred. No. 2e-81;
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                                                                                Julia E.
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Johnston, Gross, Jane A.

Janet V.

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CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2
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PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10282622
Publication No. US20030134390A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: No. US20030134390A1ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
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                                                                                                                              Matches
                                                                                                                                                                       Query Match
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/295,723
                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                Match 100.0%; Score 850; DB 4
Local Similarity 100.0%; Pred. No. 2e-81;
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                                                                                                                              162;
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                                          1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60
  LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
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100.0%; Pred. No. 2e-81;
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US-10-456-780-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10456780 Publication No. US20040009150A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10659684
Publication No. US20040110932A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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APPLICANT: Hammond, Angela K.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/10/659,684

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547

PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-09

PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Novak, Julia E.
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TYPE: PRT
ORGANISM: Homo sapiens
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
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                                                                                                                                                                                                                                                                                                             Gross, Jane A.
                                                                                                                                                                                                                                             Nelson, Andrew J.
Dillon, Stacey R.
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100.0%; Pred. No. 2e-81;
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APPLICANT: Grusby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Young, Deborah
INTERMIT APPLICANT: Whitters, Mary
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
TITLE OF INVENTION: Cell Development and Function
FILE REFERENCE: 22058-85
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
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LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-684-2
RESULT 10
US-10-872-087-10
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Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches
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Local Similarity 100.0%; 1
nes 162; Conservative 0;
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                                                                                                                                                                                            LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
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Pred. No. 2e-81;
, Mismatches 0; Indels
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APPLICANT: JOHNSTON, JUNET V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: NUMBER: US/10/787,442
CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-07-01
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PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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Best Local Similarity
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Publication No. US20040235743A1
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APPLICANT:
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APPLICANT:
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version
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APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/872,087
CURRENT FILING DATE: 2004-06-18
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TYPE: PRT
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Julia E.
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Pred. No. 2e-81;
Mismatches
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APPLICANT: Nelson, Andrew
ITITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
ITITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
ITITLE OF INVENTION: USING IL-21
IFILE REFERENCE: 03-09
CURRENT APPLICATION NUMBER: US/10/951,239
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/505,919
PRIOR FILING DATE: 2003-09-25
INUMBER OF SEQ ID NOS: 10
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
                                                                                                                                                                                                            RESULT 13
US-10-775-204-2177
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US-10-951-239-2
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                                                                                                                                               Sequence 2177, Application US/10775204 Publication No. US20050186664A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 850; DB 5
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches
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Best Local Similarity
                 APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
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APPLICANT: Nelson, Andrew
CURRENT APPLICATION NUMBER: US/10/775,204
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                            TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
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100.0%; Pred. No. 2e-81;
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CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
ELNGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-11-174-398-2
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; ORGANISM: Homo sapiens
US-10-775-204-2177
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2177
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Publication No. US20050244930A1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
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PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
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PRIOR ETILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
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PRIOR APPLICATION NUMBER: 60/378,950
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PRIOR FILING DATE: 2002-11-05
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PRIOR FILING DATE: 2002-10-02
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100.0%; Pred. No. 2e-81;
ative 0; Mismatches
100.0%;
  Score 850; DB 6
Pred. No. 2e-81;
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                          Length 162;
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Sequence 2, Application US/11134489

Publication No. US20050265966A1

GENERAL INFORMATION:

APPLICANT: Kindsvogel, Wayne R.

APPLICANT: Holly, Richard D.

APPLICANT: Clegg, Christopher H.

APPLICANT: Foster, Donald C.

APPLICANT: Heipel, Mark D.

APPLICANT: Heipel, Mark D.

APPLICANT: L....Sivakumar, Pallavur V.

APPLICANT: Of INVENTION METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY THE REFERENCE: 04-03

CURRENT APPLICATION NUMBER: US/11/134,489

CURRENT FILING DATE: 2005-05-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens
Search completed: September Job time : 59.2829 secs
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US-11-134-489-2
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                                                                       121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
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                                                                                                                                                                        61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
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                   7, 2006, 12:57:58
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                        protein search, using
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Match
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Gapop 10.0 , Gapext 0.5
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1143.601 Million cell updates/sec
  Published_Applications_AA_New:*

| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*
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| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US11_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US01_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/1/pubpaa/US01_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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                   US-10-511-937-2572
US-10-35-149-2
US-10-806-611-10
US-11-429-276-2167
US-10-806-611-2
US-10-806-611-12
US-10-806-611-13
US-10-806-611-13
US-10-806-611-43
US-10-806-611-43
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US-11-056-3558-3635
US-10-953-349-18970
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Sequence 2, Appli
Sequence 10, Appl
Sequence 2177, Ap
Sequence 2167, Ap
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  12, Appl
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24, Appl
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US-10-511-937-2572
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417	335	247	212	932	932	923	707	653	861	720	352	864	694	631	555	461	461	436	436
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
4863, Ap	4864, Ap	56995, A	4865, Ap	18, Appl	17, Appl	41603, A	3241, Ap	52519, A	73, Appl	51542, A	81843, A	79969, A	36372, A	79970, A	79971, A	64210, A	32619, A	•	32620, A

ALIGNMENTS

Sequence 2572, Application US/1051197 Publication No. US20060088036A1 APPLICANT: EXPRESSION DIAGNOSTICS, INC. APPLICANT: NOORMATION: AND STATE OF THE METHOD STATE OF THE METHOD STATE OF THE PRINCIPLE OF THE P
pplication US/10511937 US2006008836A1 ION: ESSION DIAGNOSTICS, INC. lemnth, Jay Kirk dward, Robert Myoc ntice, James ris, MacDonald enberg, Steven 1008 METHODS AND COMPOSITIONS FOR DIAGNOSING 1008: METHODS AND COMPOSITIONS FOR DIAGNOSING 1008: METHODS AND COMPOSITIONS FOR DIAGNOSING 1008: AND MONITORING TRANSPLANT REJECTION 1008-100104 1009: AND MONITORING TRANSPLANT REJECTION 1008-100104 1009: AND MONITORING TRANSPLANT REJECTION 1008-100104 1009: AND MONITORING TRANSPLANT REJECTION 1008-1009: 1009-1009-1009-1009-1009-1009-1009-1009

US-10-735-149-2

Sequence 2, Application US/10735149 Publication No. US20060134754A1

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Sequence 10, Application US/10806611

Publication No. US20060159655A1

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING ACONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16159-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT APPLICATION NUMBER: US 60/456,920
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR PILING DATE: 2003-03-21
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                                                                                                                                                       ; ORGANISM: Homo sapiens US-10-806-611-10
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US-10-806-611-10
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; ORGANISM: Homo sapiens
US-10-735-149-2
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APPLICANT: Chan, Chung
APPLICANT: Camost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
                                                                    Matches 162;
                                                                                      Query Match
Best Local Similarity
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Best Local
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LENGTH: 162
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CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                 LENGTH: 162
TYPE: PRT
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1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
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Similarity 100.0%;
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                                                                       Conservative
                                                                100.0%; Score 850; DB 6; 100.0%; Pred. No. 6.3e-75; tive 0; Mismatches 0;
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Pred. No. 6.3e-75;
); Mismatches 0;
                                                                                                          Length 162;
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US-11-429-276-2177
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NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2177
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                  Query Match
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
DELIGROUP TO TOTAL TO THE PRIOR FILING DATE: 2001-12-21
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PRIOR APPLICATION NUMBER: 60/420,246
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PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
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PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                     121 TCDSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
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TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
                                                                                          LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
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. US20060194735A1
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                                                                                                                                                                                                                                                                       100.0%; Score 850; DB 7; Length 162; 100.0%; Pred. No. 6.3e-75; tive 0; Mismatches 0; Indels
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US-11-429-276-2167
; Sequence 2167, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

TITLE OF INVENTION: Albumin Fusion Proteins

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; ORGANISM: Homo sapiens
US-11-429-276-2167
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NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2167
LENGTH: 742
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Appublication No.
                                                                  SEQ ID NO 28
                                                                                                                                                                                                                                                                                                    APPLICANT: Chan, (
APPLICANT: Zamost
APPLICANT: Covert
APPLICANT: Liu, I
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Best Local Similarity
                                                                                                                                                                    APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AD METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
                                                                               CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
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CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT FILING DATE: 2006-05-08
ORGANISM: Artificial Sequence
                                         ENGTH:
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OR FILING DATE: 2002-02-28
OR APPLICATION NUMBER: 60/378,950
OR FILING DATE: 2002-05-10
OR APPLICATION NUMBER: 60/398,008
OR FILING DATE: 2002-07-24
OR APPLICATION NUMBER: 60/411,355
OR FILING DATE: 2002-09-18
OR APPLICATION NUMBER: 60/414,984
OR APPLICATION NUMBER: 60/414,984
OR APPLICATION NUMBER: 60/417,611
OR APPLICATION NUMBER: 60/417,611
OR APPLICATION NUMBER: 60/417,611
OR FILING DATE: 2002-10-11
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                                                                                                                                                                                                                                                                                                                          Zamost, Bruce L.
Covert, Douglas C.
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40. US20060134754A1
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Pred. No. 2e-60;
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US-10-806-611-12
US-10-806-611-12
Sequence 12, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Coin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: optimized IL-21
US-10-735-149-28
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APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine
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Publication No. US20060159655A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
APPLICANT: YOUNG, DEBORAH A.
TITLE OF INVENTION: TRABTING IMMUNOLOGICAL DISORDERS USING AGONISTS
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pr
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100.0%; Pred. No. 4.8e-60;
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RESULT 10
US-10-806-611-4
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US-10-806-611-12
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APPLICANT: COllins, Mary
APPLICANT: Colin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
                                                                                                                                                                                                                                                                                                                                  Matches
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LENGTH: 146
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Best Local Similarity 80.3%;
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SEQ ID NO 12
LENGTH: 122
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/456,920 PRIOR FILING DATE: 2003-03-21
                                                                                                                                                                                                                                                                                                                                                      / Match 57.2%;
Local Similarity 63.0%;
                                                                                   121 YEKRTPKEFLERLKWLLQKMIHQHLS 146
                                                                                                           128 YEKKPPKEFLERFKSLLQKMIHQHLS 153
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; Pred. No. 8.9e-40;
23; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                  31; Indels
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APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US/01/2946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTMARE: PATENTIN VETSION 3.2
TYDE: DET
TYDE: DET
TYDE: DET
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; ORGANISM: Homo sapiens US-10-511-937-2499
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publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 122
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Publication No. US20060159655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                 TYPE: PRT
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Local Similarity 62.0%; Pred. No. 5.7e-31;
hes 75; Conservative 19; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wohlgemuth, Jay
Fry, Kirk
Woodward, Robert
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Query Match Best Local Similarity

11.7**%**; 25.9**%**;

Score Pred.

99.5; DB No. 0.025;

6

Length 162;

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                                                                                                  RESULT 13
                 Sequence 77, Application US/11251208 Publication No. US20060137043A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION NUMBER: 10/775,204
PRIOR FILING DATE: 2004-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT FILING DATE: 2006-05-08
APPLICANT: Puzio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PF564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 60
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US02/40891 FILING DATE: 2002-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2002-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/414,984
FILING DATE: 2002-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/360,000 FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/417,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/411,355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/420,246
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                                                                                                                                                              190
                                                                                                                                                                                                                                               130 RDHEHTSIKPEPEETCKLLKEHPDDLLSAFIHEEARNHPDLYPPAVLALTKQYHKLAEHC 189
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                                                                                                                                                                                                                                                                                      89 TGNNERII----NVSIKKLKRK----
                                                                                                                                                                                                                                                                                                                                                                  44 DIVDOLKNYVNDLVPEF------LPAPEDVETNCEWSAFSCF----QKAQLKSAN 88
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                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                              n 9.6%; Score 82; DB 7; Length 605; Similarity 24.2%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                              EINDFAKSCINDKTPECEKPVGTLFFDKLCADPAVGVNYEWSKECCAKQDPERAQCFKAH
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                                                                                                                                                                                                    CDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSED 161
                                                                                                                                                              CEEEDKE - - KCFSEKMKQLMK - - -
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    See File Wrapper or

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US-11-056-355B-36356
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                                                                                                                               CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 36356
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36356, Application US/11056355B Publication No. US20060150283A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                           APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
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PRIOR FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: EP 03008080.8
PRIOR FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: EP 03009728.1
PRIOR FILING DATE: 2003-05-02
PRIOR FILING DATE: 2003-05-02
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CURRENT FILING DATE: 2005-10-14
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TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharomyces cerevisiae
                                                              ORGANISM: Arabidopsis thaliana
                                                                                     TYPE: prt
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NAME/KEY: peptide
LOCATION: (1)..(431)
                                                                                                              ENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKNLFDRSHSN 161
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Pred. No. 33;
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APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT FILING DATE: 2005-02-14
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 45283
LENGTH: 431
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(431)
OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-3558-45283
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Search completed: September Job time: 10.9514 secs
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US-11-056-355B-45283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-36356
                                                                                                                                                                                                                                                                                                                         Query Match 8.8%; Score 74.5; DB 7; Length 431; Best Local Similarity 21.8%; Pred. No. 22; Matches 26; Conservative 24; Mismatches 48; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45283, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                      268 KVIDNINFRNFLELVPDVRELINDFYSSRYASC------LEYLASLKSNLLLDIHLH 318
                                                                                                                                                                                                               220 KYKLAARKFLDVNPELGNSYNEVI-----APQDIATYGGLCALAGFDRSELK------Q 267
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                                                                                                                                                            94 RII-NVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQH 151
                                                                                                                                                                                                                                                                     34 RHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNE 93
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A_Geneseq_8:*
1: geneseqp198
2: geneseqp200
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6: geneseqp200
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2958
1 MPRGWAAPLLLLLLQ
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	ω	2	_	Result
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ADS82585	ADP19844	ADL91861	ADM83456	ADJ25623	ADH10505	ADI01021	ADH44685	ADG87460	ABW00881	ABU62888	AAE14939	ABR61402	AAU11978	AAE13726	AAU11912	ABB81960	AAB48001	AAY79312	AAY69886	AAY45031	AAB18634	AAY27450	ID
Ads82585 Interleuk	Adp19844 Human zal	Adl91861 Human PRO	Adm83456 Human zal	Adj25623 Human int	Adh10505 Human int	Adi01021 Immunity-	Adh44685 Human Zal	Human	Abw00881 Human cyt	Abu62888 Human MU-	Aae14939 Human int	Abr61402 Human IL-	Aau11978 Human zal	Aae13726 Human sol	Aaul1912 Human MU-	Abb81960 Human 164	Aab48001 Human IL-	Aay79312 Human cyt	Aay69886 Human hae	Aay45031 HUMAN Orp	Aab18634 A human z	Aay27450 Human MU-	Description

This represents a MU-1 hematopoietin receptor protein. The protein can be produced by standard recombinant methodology. The MU-1 protein has the biological activity of the MU-1 hematopoietin receptor superfamily chain. It is used to screen for specific binding agents, to raise specific antibodies; as assay reagents, tissue markers etc. and therapeutically (optionally expressed from the MU-1 gene by gene therapy). Many possible activities/uses of the MU-1 protein are described without supporting evidence, e.g. they regulate cell proliferation and differentiation, induce production of cytokines, stimulate or suppress an immune response

Claim 9; Page 33-35; 37pp; English.

New nucleic acid encoding the MU-1 hematopoietin receptor protein, used for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.

WPI; 1999-562115/47.

N-PSDB; AAZ07535.

45	44	43	42	41	40	39	38	37	36	35	3. <u>4</u>	IJ J	32	31	30	29	28	27	26	25	24
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64.2	95.2	95.2	95.2	95.2	96.4	98.2	99.2	99.8	99.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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AAY69883	AAE13738	AAU08729	AAE02457	AAY94305	ADY54825	AAY69888	AAE02459	AAU08728	AAY94304	AEG05256	AEE19676	ADZ20509	ADZ12787	ADZ12785	ADY54732	ADY20089	ADY17690	ADY17832	ADV96468	ADS41470	ADS19027
Aay69883 Human hae	Aae13738 Human sol	Aau08729 Human HNO	Aae02457 Human DNA	Aay94305 Human HNO	Ady54825 Human zal	Aay69888 Mouse hae	Aae02459 Human DNA	Aau08728 Human HNO	Aay94304 Human HNO	Aeg05256 Human IL-	Aee19676 Human int	Adz20509 Human int	Adz12787 Human can	Adz12785 Human can	Ady54732 Human zal	PR(PRO	PR	Adv96468 Human rec	Ads41470 Human hae	Ads19027 Mature hu

ALIGNMENTS

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MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy; cell proliferation; cytokine production; immune response; cancer; autoimmune disease; transplant rejection; hematopoiesis; anemia; gene mapping; nutritional supplement; human.
                                                                                                                                                                           17-MAR-1999;
                                                                                                                                                                                                                                                                        Human MU-1 hematopoietin receptor protein.
                                                                                                                                                                                                                                                                                       26-NOV-1999
                                                                                                                                                                                                                                                                                                     AAY27450;
                                                                                                                                                                                                                                                                                                                   AAY27450 standard;
                                                                                                                               Donaldson D,
                                                                                                                                                            17-MAR-1998;
                                                                                                                                                                                          23-SEP-1999
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                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                              (GEMY ) GENETICS INST INC.
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Matches
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                                                                                                                                                           A human
             09-MAR-2000; 2000WO-US006067
                                                                                                                   tumourigenesis;
                                                                                                                                 zalphall ligand;
                                                                                                                                                                                       22-JAN-2001
                                                                                                                                                                                                                                         AAB18634 standard;
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                                        14-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                 LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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                                                                                                                                                                                                                                                                                                                           PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS
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llarity 100.0%;
Conservative 0
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                                                                                                                      ; cytokine;
leukaemia;
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Pred. No. 7.5e-240;
; Mismatches 0;
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AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS

480

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SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD

SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGI

LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG

LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL

LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG

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                                                                                                                                                                                                                                     Matches
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Best Local
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11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                   prevention, an
genetic defect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-565600/52
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          181
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                                                                                                                                                                    MPRGWAAPLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                                             APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                       EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                        EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKF
RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                           APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                                                                                                                                                                                    538 AA;
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Johnston
                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00264908.
99US-00265992.
99US-0142013P.
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                                                                                                                                                                                                                                                      Score 2958; DB 3; Pred. No. 7.5e-240;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Matches 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph nodes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10-A or its agonist can be used in the treatment of endocrine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New HUMAN orphan cytokine receptors 10 and 10-A useful for drugs e.g. receptor agonists that may mediate survival and differentiation in cells naturally expressing the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Page 39-41; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masiakowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000.
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RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                               RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                   EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                                                                                                                                                                                                                               MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
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                                                                                                                                              APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS 180
                                                                                                                                                                                                                                                     EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                                                                                                                                                                                                       MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                                                                              APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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                                                                                                                               This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are us for the diagnosis of blood formation disorders. Compounds identified a binding to the proteins are used for the treatment of such disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-2000
                                                                                                            Sequence
                                                                                                                                                                                          Claim 4;
                                                                                                                                                                                                               Hemopoietin receptor formation disorders.
                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                       24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human haemopoietin receptor family member NR8gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY69886
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                                                                            Similarity
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                                 MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVLCILEMWNLHPSTLTLTUQDQYEELKD
                                                                                                                                                                                         Fig 9-10; 176pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS
EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
                      MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
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Pred. No. 7.5e-240;
Mismatches 0;
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27(c)"
267. .273
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214. .:
                                                                                                                                                                                                                                                                       /note= "mature protein; a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)" 20...237
                                                                                                                                                                                                                                     /note= "cytokine-binding domain; a polypeptide comprising this domain is specifically claimed in Claim 27(a)"
                                                                               256. .538
/note= "intracellular signalling domain; a polypeptide
comprising this domain is specifically claimed in Claim
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                                            note=
                                                                                                                                             /note= "transmembrane domain"
                                                                                                                                                                            /note= "WSXWS
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APPFNVTVTESGOYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS

EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP

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1 MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD

Matches 538;

Conservative

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Gaps

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RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL

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The present sequence is that of zalphall, a novel human class I cytokine creciptor that may be involved in an apoptotic cellular pathway, or is a cell-cell signalling molecule, growth factor receptor, or extracellular cmatrix associated protein with growth factor hormone activity. The spinal cord library. Polypeptides comprising amino acids 20-237, 20-255, 20-358, 20-538 and 1-538 of the present sequence are claimed. Zalphall is expressed in lymph node, peripheral blood leucoytes, spleen and chymus. The manka is also abundant in the Raji cell line (ATCC CCL 86) cderived from Burkitr's lymphoma. Zalphall polypeptides, and fusion proteins including them, can be obtained by expression in recombinant thost cells. They are used: to detect ligands (also ligand agonists and can tagonists) that stimulate proliferation and/or development of the areplacement for serum in culture media; in soluble form to block ligand cartivity (direct antagonists) and to detect ligand-expressing cancers; to raise specific antibodies; and for purification of cognate ligands. Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating cartivity of vaccines, suppressing tumours, treating leukopenia and comproving The samulate cell-mediated immunity, e.g. for treating care set in section as secociated with immunosuppression, improving the associated with immunosuppression, improving the cartivity of vaccines, suppressing the marrow transplant. Antagonists of disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to prevent transplant rejection and to treat T-cell leukemia or lymphoma company transplant rejection and to treat T-cell leukemia or lymphoma company transplant rejection and to treat T-cell leukemia or lymphoma company transplant rejection and to treat T-cell leukemia or lymphoma company transplant tr
                                                                            Query Match
Best Local Similarity
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09-MAR-1999;
06-JUL-1999;
                                                                         Sequence 538 AA;
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N-PSDB; AAZ94533, AAZ94534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27(e); Page 148-149; 190pp; English
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99US-00265117.
99US-00347930.
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100.0%; Score 2958; DB 3; 100.0%; Pred. No. 7.5e-240;
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          The invention relates to isolated human and murine interleukin-9 (IL-9), IL-2 receptor-like polypeptides. The plasmid containing the encoding cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like polypeptides (16445 proteins) can be recombinantly produced using standard recombinant methodology. The 16445 proteins are used for identifying their modulators and for diagnosis and treatment of immune, inflammatory and respiratory disorders and disorders associated with lungs, colon, kidney and lymphoid tissues including tonsil and thymus, particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000;
                                                                                                                                                                     Claim 8; Page 104-106; 119pp;
                                                                                                                                                                                                               Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for diagnosis and treatment immune, inflammatory and respiratory disorders
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                                                                                                                                                                      English.
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PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPPLSSPGPQAS
                                                               AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
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                                                                                                                                                                                                                                                                                                                                                                            APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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                                                                                                           SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
                                                                                                                                                                            LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
                                                                                                                                                                                               LELGPWS PEVPSTLEVYS CHPPRS PAKRLQLTELQEPAELVES DGVPKPS FWPTAQNS GG
                                                                                                                                                                                                                                            LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                            AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
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Pred. No. 7.5e-240;
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PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS

ABB81960 standard; protein; 538

25-NOV-2002 entry)

Human 16445 protein

RESULT 7
ABB8190
IID ABB88
XX ABB88
XX ABB88
XX INTER
DE Huma
XX Inter
KW Inter
KW anti
KW anti
KW anti
XX anta
XX Inter
KW anti
XX Anthology
PN US20 Interleukin; IL-9; IL-2; 16445; antiasthmatic; antiallergic; hum antipporiatic; antiinflammatory; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; antithyroid; dermato nephrotropic; antibacterial; tuberculostatic; antileprotic; anti gene therapy; receptor. dermatological;

US2002090680-A1

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cc polypeptide, 16445. The 16445 polypeptides can be expressed by standard cc recombinant methodology. The 16445 polypeptide, polypucleotides and their cc modulators are useful for modulating the immune, inflammatory and cc respiratory responses, for the diagnosis and treatment of immune and cc respiratory disorders, particularly the immune, inflammatory and cc respiratory disorders, including, atopic conditions, such as cc lymphocyte-related disorders, including, atopic conditions, such as cc asthma and allergy, including allergic rhinitis, psoriasis, the effects cof pathogen infection, chronic inflammatory diseases, organ-specific cc autoimmunity, graft rejection, and graft versus host disease. The collectules are also useful as modulating agents in a variety of cellular cc independent proliferation of T helper cell clones, and direct effects on crall haemopoletic progenitors, human T cells, B cells, thymocytes, chymic lymphomas and neuronal cell lines. They are useful for the condulation, diagnosis, and treatment of immune, inflammatory, and creppiratory disorders and disorders associated with lungs, colon, kidney, and lymphoid tissues including tonsil and thymus. The present sequence crepresents a human 16445 polypeptide
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-655832/70.
N-PSDB; ABQ79536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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18-MAY-2000; 2000US-00574100.
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                                                                                                                                                                                                   RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                                                                                            APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                                                                                                                                                                                                        EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                               MPRGWAAPLILLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
 SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
                                   LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
                                                                                                          LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS
                                                                                                                                                                                RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                                                                     APPFNVT
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                                                                                                                                                                                                                                                    VTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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Pred. No. 7.
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7.5e-240;
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RESULT 8
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XX AAUL
XX Huma
XW Huma
XW Huma
XW Syst
XW Pulm
XW Pulm
XX Homc
XX Hom
XX Ho
The present invention relates to a new murine MU-1 protein, a CC haematopoietin receptor superfamily chain, comprising a fully defined CC sequence of 529 amino acids (AAUJ1915) as given in the specifications or CC fragment of protein having MU-1 biological activity. The molecules of the CC invention may exhibit cytokine, cell proliferation or cell convention activity and may also exhibit immune stimulating or CC immune suppressing activity and can be useful in the treatment of various immune deficiencies and disorders including severe combined CC immunodeficiency (SCID). Another use of the invention is treating CC sulcommune disorders such as connective tissue disease, multiple CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune CC is useful for the treatment of mysloid arthritis, insulin dependent CC is useful for the treatment of mysloid or lymphoid cell deficiencies and cin treating various anaemias or for use in conjunction with cCC irradiation/chemotherapy to stimulate the production of erythroid can procursors and/or erythroid cells. The polynucleotides and proteins can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, useful for identifying compounds binding to MU-1, for treating multiple sclerosis, rheumatoid arthritis, diabetes and asthma, comprises the isolated murine MU-1 protein, and a hematopoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis; immune deficiency; anaemia; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; pulmonary inflammation; insulin dependent diabetes mellitus; nutritional supplement; cytokine receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                            Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents the human MU-1 haemopoietin receptor superfamily chain. MU-1 is also a member of the cytokine receptor family. This sequence was used in the invention for the characterisation of previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also be used as nutritional sources or supplements. The present protein
                               Protein
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                         /label= Signal_peptide
/label= Mature_Zalphal1_protein
                                                                                                            Location/Qualifiers
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180 120

EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP

APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS

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Best Local 9
                                                                                                                                                                                                                                                                    lymphoid cells which are natural killer cells or cytotoxic T cells. Zalpha is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphall cytokine receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their cDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoietic cells and haematopoietic cell progenitors preferably lymphoid cells which are natural killer cells or cytotoxic T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000;
28-JUL-2000;
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                                                                                                                                                                                                                                Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 172-173; 243pp; English.
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EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                          MPRGWAAPLILLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                                                                                                                               Conservative
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2000US-0222121P.
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/note= "Box II signalling site"
519. 522
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120. .123
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                                                                                                                                        Score 2958; DB 5;
Pred. No. 7.5e-240;
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11-MAR-1999;
01-JUL-1999;
The present invention relates to the isolation of a novel cytokine, zalphall Ligand and the polynucleotide encoding it. The invention algives the sequence for the zalphall receptor and the polynucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation natural killer (NK) cells or NK cell progenitors, the activation of
                                                                                                                                                                                                             New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or of inhibition of specialized cell function, or for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system;
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                                                                                                                                         Claim 1; Col 191-194; 105pp; English.
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                                                                           arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R; immune cell activity; cancer; infectious disorder; antirheumatic; antiparterial; antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacterial; virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological; neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic;
                           neuroprotective; antiulcer; ant antithyroid; antiinflammatory; autoimmune disease; human.
                                                                                                                                                                                                                                                                                         12-AUG-2003
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Pred. No. 7.5e-240;
; Mismatches 0;
                                                        immune response;
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Homo sapiens

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The invention relates to a novel method for treating or preventing an CC arthritic disorder in a subject. The method involves administering to the Subject an interleukin-21 (II-21)/II-21 receptor (II-21R) antagonist CC optionally in combination with another therapeutic agent, to inhibit or CC treating or preventing cancer or an infectious disorder, in a subject, by CC administering II-21/II-21R agonist, to increase immune cell activity. The CC method of the invention has antirheumatic, antiarthritic, osteopathic, CC immunosuppressive, antidiabetic, neuroprotective, dermatological, CC antilulcer, antiasthmatic, antiallergic, antianaemic, hepatotropic, CC treating or preventing an arthritic disorder such as rheumatoid CC arthritis or ankylosing spondylitis, and also cancer such as solid CC arthritis or ankylosing spondylitis, and also cancer such as solid CC tumour, soft tissue tumour or metastatic lesion, or an infectious CC disorder such a bacterial, viral or parasitic infection in a mammal, CC preferably human. A method of the invention is also is useful for CC increasing the ability of a vaccine composition containing an antigen to increasing the ability of a vaccine composition containing an antigen to CC elicit a protective immune response in a subject against the antigens. Or from cancer or tumour cell antigen, or expressed on the surface of cancer CC cell. An alternative method of the invention is useful for modulating the ccitivity of immune or haematopoietic cells and thus to treat or prevent a ctivity of immune or haematopoietic cells and thus to treat or prevent a chievent of concernatitis, unlergy, asthma, allergic asthma, anaemia, anaemia, CC hepatitis, Graves's disease, graft versus host disease, and scleroderma. The present sequence is used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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N-PSDB; ACC80861.
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17-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 538
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APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                             EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
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2002US-0373746P
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Pred. No. 7
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Ma M,
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7.5e-240;
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Witek JS,
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5 밁 ঠ 밁 ঠ

The invention relates to polynucleotides and polypeptides of interleukin21 (II-21) antagonists, that bind with specificity and exhibit an EC50
that is not detectable in receptor binding studies. The antagonists of
the invention have mutations in the D helix of the II-21 molecule, and
can be used to inhibit the activity of II-21 with its cognate receptor.
The II-21 antagonists are useful for diagnosing and treating disorders
involving the abstrant expression or activity of the II-21 polypeptide,
such as cancer, inflammatory and autoimmune disorders, including

cancer, intla

New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and

N-PSDB;

AAD47859

Example 1;

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71pp;

English

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Best Local :
                                                                                                                                                                                                                 Human; MU-1; haematopoietin receptor superfamily chain; immunom cytostatic; antibacterial; virucide; antianaemic; gene therapy; haematopoieesis; anaemias; immune response; cancer; infection; transplanted organ; cytokine; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 receptor (originally designated zalphall receptor)
17-MAR-1998;
28-APR-2000;
                                                         04-OCT-2001;
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Pred. No. 7.5e-240;
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SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD

420

LELGPWS PEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG

360 300 300 240

LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG

LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPPTGSS

LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS

RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL

RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL

APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS

APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS

180

120

60

0

481 421 421

PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS 480

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                      The invention describes a fusion polypeptide comprising at least a fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The polypeptide is useful in regulating haematopoiesis (e.g. in cases of anaemias) and/or immune responses (e.g. immune response to cancer, infections or to a transplanted organ) and in identifying other members of the haematopoietin superfamily, including cytokines and receptore. The polymucleotide may be used to express recombinant protein for analysis, characterisation or therapeutic use; and as markers for tissues or characterisation or therapeutic use; and as markers for be used as mutritional sources or supplements. This is the amino acid sequence of human MU-1 haematopoietin receptor superfamily chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion polypeptide for regulating hematopoiesis and immune recomprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide.
                                                                                                                                                                                                                                                                   Sequence 538
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N-PSDB; ACD26717.
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RESULT 14
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                                         The invention relates to a cytokine receptor designated Zalphall and its nucleic acid sequence. Zalphall protein is useful for detecting ligands that stimulate the proliferation and/or development of haematopoietic, lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful in identifying a region of the genome associated with human disease states. Zalphall protein is useful for treating lymphoid, immune, inflammatory, spleenic, blood or bone disorders. The present sequence in
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RESULT 15
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                                                                                                                                                /label= Signal_peptide
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                                                                                 "Domain
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             Complete
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Pred. No. 7
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Query Match
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Matches 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 538 AA;
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> Search completed: September Job time : 226.886 secs 2006, 12:44:55

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ALIGNMENTS

R;Hatakeyama, M.; Tsudo, M.; Minamoto, S.; Kono, T.; Doi, T.; Miyata, T.; Miyasaka, M.; Science 244, 551-556, 1989
A;Title: Interleukin-2 receptor beta-chain gene: generation of three receptor forms by A;Reference number: A30342; MUID:89242117; PMID:2785715

S.; Kono, T.; Doi, T.; Miyata, T.; Miyasaka, M.;

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A;Cross-references: UNIPROT:P14784; UNIPARC:UPI00000128F; GB:M26062; NID:g186322; PIDN

A; Molecule type: mRNA A; Residues: 1-551 <HAT>

A; Accession: A30342

C;Date: 31-Mar-1990 C;Accession: A30342

N; Alternate names: CD25 beta chain

Species: Homo sapiens (man) ;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

interleukin-2 receptor beta chain precursor -

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A;Map position: 22q11.2-22q13
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type II: C;Keywords: cytokine receptor; transmembrane protein F;1-26/Domain: signal sequence #status predicted <SIG> F;27-551/Product: interleukin-2 receptor beta chain #status predicted
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A;Cross-references: GDB:118822; OMIM:146710
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                                                                                                                 WSDPVIPOTQSEELKEG---WNPHLLLLLLLVIVFIPAFWSL----KTHPLWRLW-KKIW 268
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  KCNTPDPSKFFSQLSSEHGGDVQKWLSSPFPSSSFSPGGLAPEI-SPLEV---
                                           A--VPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGPWSPEVPSTLEVYSCHPPRSPA 326
                                                                                   WSQPLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGP----WLKKVL
                                                                                                                                                                         EARTLSPGHTWEEAP---LITLKQKQEWICLETLTPDTQYEFQVRVKPLQGEF--TTWSP 222
                                                                                                                                                                                                                  ELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSE 216
                                                                                                                                                                                                                                                                                                                                                   ALQD--TSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLC 110
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26.0%; Pred. No. 3.8e-12;
tive 75; Mismatches 199
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Un-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C;Accession: B46535
R;Page, T.H.; Dallman, M.J.
Bur. J. Immunol. 21, 2133-2138, 1991
By: J. Immunol. 21, 2133-2138, 1991
A;Title: Molecular cloning of CDNAs for the rat interleukin 2 receptor alpha and A;Reference number: A46535; MUID:91364784; PMID:1889461
A;Accession: B46535
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A;Residues: 1-537 <PAGE
A;Crose-references: UNIPARC:UPI000017987A
A;Crose-references: UNIPARC:UPI000017987A
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:60816, NCBIP:60819)
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: cytokine receptor
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;Species: Rattus norvegicus (Norway rat)
;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.4%;
Best Local Similarity 23.5%;
Matches 148; Conservative
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                                                 407 GLEP-----
                                                                                                                                           354 TAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTW----PC---SCEDDGYPALDLDA 406
                                                                                                                                                                                                                                                                                              266 LVKCRYLGPWLKTLLKCH------IPDPSEFFSQLSSQHGGDLQKWLSSPVPQSF 314
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PLPPLLPFTGEQDDYCAFPPRDDLLL-
                                                                                             --GHSQASCFTNQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                     QVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLLLLLLVIVFIPAFWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVCWEEKGWRRVKTCNFHPFDNLRLIAPHSLQVLHIETRRCNISWEVSQVSHYVNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIT--DQSGNYSQECGSFLLAESIKPAPPFNVTVTF--SGQYNISWR----SDYEDPAFY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PEEALNVTSCHIHAKSDMRHWNKTCELTFVRQASWACNLILGFLPDSQSLTSVDLLSL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELKDEA---TSCSLHRSAH----NAT-----HATYTCHM-----DVFHFMADDIFSV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAAPL--LLLLQGGW-----GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 56
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                                                                                                                                                                                                                                           ---TGSSLELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWP 353
                                                                                                                                                                                                                                                                                                                                             -----EKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPF----
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                                              -SPGLEDPLLDAGTTVLSCGCVSAGSPGLGGPL----GSLLDRL 449
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                                                                                             -GYFFFHLSNALEIESCOVYFYYDPCMEEDVEEDG-PRLPEES
- FSPSLSTPNTAYGNSITPEE
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453 LADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMD 488 	372GLVSIDTVTVLDAEGPCT	ω—ω × ·	99 TDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSQQYNISWRSDYEDPAFYML 150	5 WAAPLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 56	A35052 interleukin-2 receptor beta chain precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004 C;Accession: A35052 R;Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Minamoto, S.; Tsudo, M.; Miyasaka, M.; M Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990 A;Title: Murine interleukin 2 receptor beta chain: dysregulated gene expression in lymphk A;Reference number: A35052; MUID:90175385; PMID:2155425 A;Ratus: preliminary A;Molecule type: mRNA A;Residues: 1-539 <kon> A;Residues: 1-539 <kon> A;Residues: uniproT:P16297; UNIPARC:UP10000003F26; GB:M28052; NID:g198313; PIDN:J C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology C;Keywords: cytokine receptor; transmembrane protein Query Match Best Local Similarity 23.7%; Pred. No. 5.5e-10; Matches 138; Conservative 68; Mismatches 198; Indels 179; Gaps 29;</kon></kon>	450 KPPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMDTFDSGFVGSDCSSPVECDFTS 509

RESULT 4

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A;Molecule type: mRNA
A;Residues: 1-896 <GOR>
A;Residues: 1-896 <GOR>
A;Cross-references: UNIPROT:P26955; UNIPARC:UPI0000027E85; GB:M34397; NID:g191821; C;Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 rec;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor; Keywords: cytokine receptor; duplication; transmembrane protein
C;Keywords: cytokine receptor; duplication; transmembrane protein
F;1-22/Domain: cytokine receptor common beta chain #status predicted <AIG>
F;23-896/Product: cytokine receptor common beta chain #status predicted <AIT>
F;39-235/Domain: cytokine receptor homology <CRS1>
F;39-235/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: transmembrane #status predicted <INM>
F;464-896/Domain: intracellular #status predicted <INM>
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A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protei A;Reference number: A35782; MUID:90319131; PMID:1695379
A;Accession: A35782
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A45268
interleukin-9 receptor precursor - mcC;Species: Mus musculus (house mouse)
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R;Gorman, D.M.; Itoh, N.; Kitamura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLOCFFDGIOSLHCSWEVWTQTTGSVSFGLFYRPSPVA-----PEEKCSPVVKEP
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                                                                                                                                                                                                        IPPPLSSPGPQAS
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                                                                                                                                                                                                                                                                                                                                                                                                        TTVLSCGCVSAGSPGLGGP----LGSLLDRLKPPLADGE---DWAGGLPWGGRSPGG---
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Pred. No. 1.1e-08;
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
C;Accession: A40091; A43022
R;Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama,
Science 247, 324-327, 1990
                                                                                                      interleukin-3 receptor beta chain precursor -
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-
C;Accession: A40091; A43022
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A,Title: Cloning of an interleukin-3 receptor gene: a member of a A,Reference number: A40091; MUID:90117145; PMID:2404337 A,Accession: A40091
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A;Molecule type: mRNA
A;Residues: 1-468 <REN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNOVTEIKHKCTFWDSMCTLVLPKEEVFLPFDNFTITLHRCI---MGQE--QVSLVD--- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGVSVP-----EQGGGGQKAGAFTCLSNSIYRIDC-----HWSAPELGQESRAWLLFT 83
                                                                                                                                                                                                                                                                                                                        DSGFVGSDCSSPVECDFTS-PGDEGPPRSYLROWVVIP
                                                                                                                                                                                                                                                                                                                                                                     ELEGOPSAYLP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAVATLTYSPACPVQFACLKWEATAPGFPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTVTVLDAEGPCTWPCSC-----EDDGYPALDLDAGLEPSPGLEDPLLDAGTTVLSCGCV 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SQYLPRRHIKLDPPSDLQSNVSSGRCVLTWGINL---ALEPLITSLSYELAFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDQYEELKDEAT----SCSLHRSAHNA----THATYTCHMDVFHFMADDIFSVNITDQSG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGWAAPLLLLLQGGWG--CPDLVCYTDYLQTVICILEMWNLHPSTLTL----TW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEEAWEARHKDRIVGV--TWLILEAVELNPGSIYEARLRVQMTLESYEDKTEGEYYKSHW
                                                                                                                                                                                                                                                                                    -SDYCMLDCCE--ECHLSAFPGHTESPELTLAQPVALP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEWSOPVSF--PSPORROGLLVPRWOWSASIL------VVVPIFLLLTGFVHLLFKLSP
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Pred. No. 3.3e-08;
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                                                                                                                               30-Jun-1993 #text_change 09-Jul-2004
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A, Status: nucleic acid sequence A, Molecule type: mRNA

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interleukin-9 receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: B45268
R;Renauld, J.C.; Druez, C.; Kermouni, A.; Houssiau, F.; Uyttenhove, C.; Van
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; c C;Keywords: cytokine receptor; duplication; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>F;3-878/Product: interleukin-3 receptor beta chain #status predicted F;33-440/Domain: extracellular #status predicted <EXT>F;99-236/Domain: cytokine receptor homology <CRS1>F;254-433/Domain: cytokine receptor homology <CRS2>F;441-462/Domain: transmembrane #status predicted <IMM>F;463-878/Domain: intracellular #status predicted <INT>
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A;Residues: 1-815,'Q', 817-878 <GOR>
A;Crooss-references: UNIPARC:UPI000020F33; GB:M29855; NID:g198342; PIDN:ANA39295.1;
C;Comment: In mice there are two classes of high-affinity IL-3 receptors. One contain
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 7.4%; Score 218.5; DB 1;
Similarity 21.5%; Pred. No. 1.2e-07;
19; Conservative 79; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKIPKYIDHTF-----QVQYKKKSESWKDSKTENLGRVNSMD---LP-QLEPDTSY
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                                                                                                                                                                                                                                  VIPPPLSSPGPQAS
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C.; Kermouni, A.; Hou
U.S.A. 89, 5690-5694,
                                                                                                                                                                                                                                                                                                                                                                                                                                ----STEQLPNVQVEGPI--PSSRPRKQLPSFDFN-----GPYLGP
                                                                                                                                                                                                                                                                                                                                                    QSHSLPDLPGQLGSPQVGGSLKPAL----PGSLEYMCLPPGGQV
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e protein
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A;Title: Expression cloning of the mul
A;Reference number: A45268; MUID:92302
A;Accession: B45268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-522 - REN>
A;Cross references: UNIPROT:Q01113; UN
A;Cross references: T-
                                                                                                                                                                                                   gene gfi-2 protein - rat
(;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul
C;Accession: 156896
R;Flubacher, M.M.; Bear, S.E.; Tsichlis, P.N.
J. Virol. 68, 7709-7716, 1994
A;Cross-references: UNIPROT:Q63216; UNIPARC:UPI00000E6943; GB:L36459; C;Genetics: A;Gene: gfi-2
                                                           A; Molecule type: mRNA
A; Residues: 1-467 < RES>
                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                    A;Accession: I56896
A;Status: preliminary; translated
                                                                                                                                            A; Reference number:
                                                                                                                                                                                  . Virol. 68, 7709-7716, 1994;Title: Replacement of interleukin-2 (IL-2)-generated
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPMTTLLSYELAFKKQEEAWEQAQHRDHIV----GVTWLILEAFELDPGFIHEARLRVQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG---PCTWPCSCEDDGYPALDLDAG--
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Pred. No. 1.1e-07;
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T-cell proliferation; transmembrar
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                                                                                                      GB/EMBL/DDBJ
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R;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, Blood 78, 2548-2556, 1991
A;Title: Cloning of the human erythropoietin receptor gene A;Reference number: A49824; MUID:92399733; PMID:1668606
A;Accession: A49824
                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P19235; UNIPARC:UPI000012A0AD; GB:M604 R;Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenk: Blood 76, 24-30, 1990 A;Title: The gene for the human erythropoietin receptor: analysis A;Reference number: A60160; MUID:90304334; PMID:2163695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 05-Apr-1995 #text_change
C;Date: 12-Feb-1999; A60160; A49824; A53958; A55280; I52563
C;Accession: A47999; A60160; A49824; A53958; A55280; I52563
R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
Blood 76, 31-35, 1990
                                                                                                                                                                                                 A;Molecule type: mRNA; DNA
A;Residues: 1-101,'R',103-188,'RP',191-243,'E',245-508 <WIN>
A;Cross-references: UNIPARC:UPI00001736C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Human erythropoietin receptor: cloning, expression, A;Reference number: A43799; MUID:90304340; PMID:2163696 A;Accession: A43799
                                                                                                                                                                                                                                                                A;Accession: A60160
A;Status: not compared with conceptual translation
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A; Experimental source: placenta
                                            A; Molecule type: DNA
A; Residues: 1-508 <N
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                     Cross-references: UNIPARC: UPI000012A0AD;
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                                              1-508 < NOG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSDLQSNVSSGRCVLTWGISF---GLEPLITSLSYELAFKRQEEAWE-QARLKDRIVGVT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLYSVYHGDFQTWIGARRAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFNV-TVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVLPKEEAFLPFDNFTITLHRCV---MGQE--QVSLVD-----SQYLPRRHIKLDP
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; Pred. No. 1.2e-07; 
61; Mismatches 179;
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                       GB:S45332; NID:g255496; PIDN:AAB23271.1;
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A;Map position: 19p13.3-19p13.2
A;Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-508/Product: erythropoietin receptor #status predicted <MAT>
F;25-250/Domain: extracellular #status predicted <EXT>
F;52-239/Domain: cytokine receptor homology <CRS>
F;23-237/Region: WSXWS motif
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A;Residues: 1-17;381-387,'LLEQQQDA',391-395;504-508 <PEN>
A;Residues: 1-17;381-387,'LLEQQQDA',391-395;504-508 <PEN>
A;Cross-references: UNIPARC:UPI000016ABA3; UNIPARC:UPI00001736C3; UNIPARC:UPI00001736C4
A;Note: sequence modified after extraction from NCBI backbone
A;Note: the authors translated the codon GAT for residue 31 as B
A;Note: an insert compared to other published sequences is considered by authors as like
A;Note: an insert compared to other published sequences is considered by authors as like
B;Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.
Blood 78, 2557-2563, 1991
A;Title: Cloning of the gene encoding the human erythropoietin receptor.
A;Reference number: 152563; MUID:92399734; PMID:1668607
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A; Residues: 1-96 < RES >
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Genomics 11, 974-980, 1991
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276 R-ALKQKIWPGIPSPESEFEGLFTTHKGNFQLWLYQNDGCLW--
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                                                                                                                                                                                                                                                                                                                                                                           QSGNYSQECGSFLLAESIKPAPPFNVTVTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                   GNYSFSYQ-----LEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVP---LELRVTA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLTLTWODOYEELKDEATS-CSLHRSAHNATHATYTCHM----DVFHFMADDIFSVNITD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLLLLQGGWGCP---
                                                  LWRLWKKIW-AVPSPERFFMPLYKGCSGDFKKWV----GAPFTGSSLELGPWSPEVPSTL 314
                                                                                                       A-RMAEPSFGGFWSAWSEPVSLLTPSD-----LDPLILTLSLILVVILVLLTVLALLSHR
                                                                                                                                                       AGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL--LLLLVIVFIPAFWSLKTHP
                                                                                                                                                                                                                 PETP----MTSHIRYEVDVSAGNGAGSV--
                                                                                                                                                                                                                                                                 YEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQVR
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9, 973-977, 1991
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                                                                                                                                                                                                                                                                                                                            ----APRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 213; DB 1;
; Pred. No. 1.5e-07;
63; Mismatches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Asn) (covalent) #status predicted
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PMID:1654273
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A;Gene: rIL-3Rbeta
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common C;Keywords: cytokine receptor
C;Keywords: cytokine receptor homology <CRS1>
F;39-235/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_cha
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_cha
C;Accession: I56563
R;Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A;Titla: Cloning of rat interleukin-3 receptor beta-subunit
A;Reference number: I56563; MUID:95370942; PMID:7643220
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C;Genetics:
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A; Residues: 1-896 < RES>
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C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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4
                                                                   GVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVL--DAEGPCTWPCSCEDDGYPAL 402
                                                                                                                                                                             --WVMPTLWIVLILVFLILTFLLALRFGCIYGCKLYRRWKEKIPNPSKSLLFQDGGKGL-
                                                                                                                                                                                          EGW-NPHL---LLLLLVIVEIPA--FWSLKTHPLWKKIWAVPSPERFEMPLYKGCS 285
                                                                                                                                                                                                                                                                              RRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELK
                                                                                                                                                                                                                                                                                                                         ESFNHIQMNPPTLNLTKN-RDSYSLHWETQKMSYPFI----QHAFQVQYKKKLDRWEDSK 390
                                                                                                                                                                                                                                                                                                                                                           LA-ESIKPAPP-FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSP 171
                                                                                                                                                                                                                                                                                                                                                                                              SSSPKAGEKKCSPVVKELQASRYTRYHCSLNVSDPAAHSQYTVSVK-----RLEQGKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                QYEELKDEATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRGWAAPLLLLLLQGGWGCP------DLVCYTDYLQTVICILEMWNLHPSTLTLTWQD
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DLDAGLEPSPGLE-DPLLDAGTTVLSCGCVSAGSPGLGGPL-----GSLLD---
                                                                                                                                                                                                                                                  TENLNHAHSMD----LP-QLEPGTSYCARVRVKTIP--EYKGLWSEWSNECTWTTD-----
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                                                                                                                                        GDFKKWVGAPFTGSSLELGPWSPEVPSTLEVYSCHP-PRSPAKRLQLTELQEPAELVESD
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                                 -GVSYTHLEDNEVSPLTIEDPNIIRDPSSGPDTTPAASSEP----
                                                                                                        -----WPP--GSTVTFSSKNPTPQGPQNNL-FSELQ------
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                                                                                                                                                                                              241
                  ASDLPTEQPPSPQPGPPAASHTPEKQASS----
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F;250-431/Domain: cytokine receptor homology <CRS2>F;444-460/Domain: transmembrane #status predicted <TMM>F;461-897/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-897 <HAY>
A;Cross-references: UNIPARC:UPI00001736C0; GB:M38275
C;Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
C;Accession: A3925
C;Accession: A3925
R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota,
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor
A;Reference number: A39255; MUID:91080571; PMID:1702217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:126838; OMIM:138981
A;Map position: 22q13.1-22q13.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: CSF2RB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 NIECFFDGAAVLSCSWEVRKEVASSVSFGLFYKPSPDAGEEECSPVLREGLGSLHTRHHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 DIVCYTDYLQTVICILEMWNLHPSTLT--LTWQDQYEELKDEATSC-----SLHRSAH-
                                                                                                                                                                                                                                                                                                                                           LLLLVIVFIPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVTFSG-QYNISW-----RSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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                                                   LTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTW
                                                                                                                             GSMSAFTSGSPPHQGPWGSRFPELEGVFPVGFGDSEVSPLTIEDPKHVCDPPSGPDTTPA
                                                                                                                                                                                                   --VGAPFTGSSLELGPWS---PEV----
                                                                                                                                                                                                                                                                     VLALIVIFLTTAVLLALRFCGIYGYRLRRKWEEKIPNPSKSHLFQ-----NGSAELWPP
                                                                                                                                                                                                                                                                                                                                                                                                                 HSMALPALE--PSTRYWARVRV-RTSRTGYNGIWSEWSEARSWDTES--VLPMW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVTKDGDSYSLRWETMKMRYEHIDHTF-----EIQYRKDTATWKDSKTETL--QNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPPVEL----KEEEQEPRDN----PVTLPISSGGPKDS
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Pred. No. 1.3e-06;
6; Mismatches 219;
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A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <WAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P14753; UNIPARC:UPI000000B997; GB:S59388; NID:g237036; PIDN:A;Experimental source: murine erythroleukemia (MEL) cell line F5-5
R;D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A;Title: Expression cloning of the murine erythropoietin receptor.
A;Reference number: A32385; MUID:89195238; PMID:2539263
A;Accession: A32385
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A32385
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A; Residues: 1-507 < KUR>
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A; Residues: 1-507 < DAA>
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A; Residues: 1-507 <HIN>
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A;Accession: A41686
                                                                                                                                                                                                                                                                                                                                           250-271/Domain: transmembrane #status predicted <TMM>;272-507/Domain: intracellular #status predicted <INT>;27-62,90-106/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                            75/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                          Matches
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                           41 NLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATYTCHM---DVFHFMADDIFSVN
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                                                                                                                                             PRGWAAPLLLLLQGGW-------GCPDLVCYTDYLQTVICILEMW
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                                                                                         PR--VGPLCLLLAGAAWAPSPSLPDPKFESKAALLASRGSEELLCFTQRLEDLVCFWE--
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                                                                                                                                                                                                    6.8%; Score 201; DB 1; ilarity 23.1%; Pred. No. 1e-06; Conservative 60; Mismatches 18
<del>..</del>
                                                                                                                                                                                                       Mismatches 188;
                                                                                                                                                                                                                                                                                                                         (covalent) #status predicted
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                                                                                                                                                                                                          Indels 142;
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A,Experimental source: PC12 and erythroid cells
A,Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBIP:132813)
C,Superfamily: erythropoietin receptor; cytokine receptor homology
C,Keywords: cytokine receptor; glycoprotein; transmembrane protein
F,1-24/Domain: signal sequence #status predicted <STG>
F,1-24/Domain: erythropoietin receptor #status predicted <MAT>
F,25-239/Domain: extracellular #status predicted <EXT>
F,25-238/Domain: cytokine receptor homology CCRS>
F,55-238/Domain: cytokine receptor homology CCRS>
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A46713
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A;Title: Functional erythropoletin receptor of the cells with A;Reference number: A46713; MUID:93266574; PMID:7684373
A;Accession: A46713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, J. Biol. Chem. 268, 11208-11216, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erythropoietin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A46713
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A;Cross-references: UNIPROT:Q07303; UNIPARC:UPI000012A0AE; GB:D13566; NID:g286209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: mRNA
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123
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                                                                                                                                                                                                                                                                                      126;
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                                                                                                                                      41 NLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATYTCHM----DVFHFMADDIFSVN 97
                                                                                                                                                                                                                                       N
VTEASGSPRYHRIIHINEVVLLDAPAGLLARRAEEGSHVVLRWLPPPGAPMTTHIRYEV- 181
                                                                                            EAANSGMGFNYSFSYQLEGESRKSCRLHQAPTVRGSMRFWCSLPTADTSSFVP---LELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVP-----KPSFWPTAQNSGGSAY- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAVRA-RMAEPSFSGFWSAWSEPASLLTASD-----LDP-LILTLSLILVLISLLLTVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYE 197
                                            ITDQSGN--YSQ-----
                                                                                                                                                                                        PR--VSPLCLLLAGAAWASSPSLPDPKFESKAALLASRGSEELLCFTQRLEDLVCFWE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGLEDPLIDAGTTVLSCGCVSAGSPGL 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAASSGMDFNYSFSYQLEGESRKSCSLHQAPTVRGSVRFWCSLPTADTSSFVP---LELQ
                                                                                                                                                                                                                                       PRGWAAPLLLLLQGGW-----
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                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                 Score 195; DB 1;
Pred. No. 2.8e-06;
0; Mismatches 194
                                            --ECGSFLLAES-
                                                                                                                                                                                                                                                                                                                                                                                  (covalent) #status
                                                                                                                                                                                                                                         -----GCPDLVCYTDYLQTVICILEMW
                                                                                                                                                                                                                                                                                    194;
                                                 ----IKPAPPENVTVTFSGQYNIS 137
                                                                                                                                                                                                                                                                                                                                Length 507;
                                                                                                                                                                                                                                                                                      Indels 198;
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285

267 205 207 159 156 101

368

386

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-74,/I',76-825 <IDZ>
A;Cross-references: UNIPARC:UPI0000044371; GB:X52425; NID:g33833; PIDN:CAA36672.1;
A;Genetics:
A;Gene: GDB:IL4R
A;Gross-references: GDB:118823; OMIM:147781
A;Gene: GDB:IL4R
A;Gross-references: GDB:118823; OMIM:147781
A;Gene: GDB:IL4R
A;Gene: GDB:IL4R
C;Superiamily: interleukin-4 receptor; cytokine receptor homology
C;Superiamily: interleukin-4 receptor; transmembrane protein
F;1-25-Domain: signal sequence #status predicted <SIG>
F;26-825/Domain: signal sequence #status predicted <MAT>
F;26-825/Domain: extracellular #status predicted <EXT>
F;34-218/Domain: cytokine receptor homology <CRS>
F;34-218/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-4 receptor precursor - human

N;Alternate names: IL-4 receptor

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: A60386; A47603

R;Galizzi, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastel

Int. Immunol. 2, 669-675, 1990
                                                                                                                         F;233-256/Domain: transmembrane #status predicted <TMM>F;257-825/Domain: intracellular #status predicted <INT>F;53,98,128,134,176,209/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 171, 861-873, 1990
A;Title: Human interleukin 4 receptor confers biological responsiveness A;Reference number: A47603; MUID:90171849; PMID:2307934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Molecular cloning of a cDNA encoding the human A;Reference number: A60386; MUID:91120547; PMID:2278997 A;Accession: A60386
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R;Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
A; Residues: 1-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.L.; March, C.J.; Mo
d. 171, 861-873, 1990
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    GWGCPDLV-
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                                           Conservative
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                                           69,
                                                              Score 193.5; DB 1
Pred. No. 6.6e-06;
                                           Mismatches
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  --CYTDYLQTVICILEMWNLHPST----L 47
                                                                                  DB 1;
                                           220;
                                                                             Length
                                           Indels
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                                                                                                                           (covalent)
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A33380
    A;Cross-references:
A:Accession: C33380
                                                                                  A;Cross-references: UNIPROT:P16382; A;Accession: B33380
                                                                                                                                                                                                                                                                                                                                    N;Alternate names: IL-4 receptor C;Species: Mus musculus (house mouse)
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                                                              A; Molecule type:
                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-810 < MO1>
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A;Accession: A33380
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                                           A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLLLLLLVIVFIPAFWSLKTHPLWRLWKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNIWSENDP------ADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAW---A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC-----GSFLLAESIKPAPPFNVTV--TFSGQYNISWRSDYEDPAFYMLKGKLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTWQDQYEELKDEATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DMDTFDSGFVGSDCSSPVECDFTS--------PGDEGPPRSYLRQWVVIP 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVPQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LEDPLLDAGTTV---LSCGCVSAGSPGLGGP---LGSLLDRLKP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDMGESCLLPPSGSTSAHMPWDEFPS----AGPKEAPPWGKEQPLHLEPSPPASPTQSPD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECEEEEEVEEEKGSFCASPESSRDD-FQEGRE---GIVARLTESLFLDLLGEENGGFCQ 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFKKWVGAPFTGSSLELGPWSP-EV-----PSTLEVYSCHPPRSPAKRLQLTELQE-P 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEPAKCPHWKNCLTKLLPCFLEHNMKRDE 322
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                       UNIPARC: UPI00001736C1
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649

NID:g198363; PIDN

VandenBos,

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	659 PSPLNSDPPKSPPECLGLELGLKGGDWVKAPPPADQVPKP 698	59	Db
	-SPGDEGPPRSYLRQWVVIPPPLSS-PGP 535	509	g 8
FTFGI	GYKAFSSLLSSNGIRGDTAAAGTDDGHGGYKPFQNPVPNQSPSSVPLFTFGLDTELS 658	602	Db
二哥	LAGLDMDTFDSGFVGSDCSSPVECDFT	482	Ş
VPGVR	PPMQPVESWEQILHMSVLQHGAAAGSTPAPAGGYQEFVQAVKQGAAQDPGVPGVRPSGDP 601	542	Дb
GVSES	451 PPLADGEDWRGGLPWGGRSPGGVSESEAGSP 481	51	γ
PSPAD	484 TLACTQVPLVLADNPAYRSFSDCCSPAPNPGELAPEQQQADHLEEEEPPSPADPHSSG 541	84	DЪ
:	TTVLSCGCVSAGSPGLGGPLGSLLDRLK	423	γQ
LSGSP	431 LAESCSPLPSGSGQASVSWACLPMGPSEEATCQVTEQPSHPGPLSGSPAQSAP 483	31	₽

Search completed: September 7, 2006, 12:52:23 Job time : 43.1971 secs

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Result
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2958
1 MPRGWAAPLULLLLQC
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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     DB
IL21R HUMAN
IL21R HUMAN
IL21R MOUSE
Q3UBSB_MOUSE
Q3UBSB_MOUSE
Q5EBB1 RAT
Q3TAB2_MOUSE
Q5FA4A CHICK
IL2RB MACFA
Q5UAP3 TETNG
IL2RB PANTR
IL2RB HUMAN
Q2UBQB BRAAR
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Q2UBQB BRAAR
Q2UBQB BRAAR
Q2TAD CAVPO
IL2RB RAT
IL2RB MOUSE
Q3TZT7_MOUSE
Q3TZT7_MOUSE
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Q4KKK7_MOUSE
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  O9hbe5 homo sapien
O9jhx3 mus musculu
O3tai3 mus musculu
O3tai3 mus musculu
O3be8 mus musculu
O5ebb1 rattus norv
O3ta82 mus musculu
O5f4a6 gallus gall
O3bj85 macaca fasc
O6uap3 tetracdon n
O38j84 pan troglod
P14784 homo sapien
O2vbq8 brachydanio
O9zla0 cavia porce
P26896 rattus norv
P16297 mus musculu
O3tztz mus musculu
O3ty715 mus musculu
O3u216 m nod-deriv
O3u114 mus musculu
O6uap7 tetracodon n
O01114 mus musculu
O78pa5 mus musculu
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	MCBI_TaxID=9606; [1] NCBI_TaxID=9606; [1] NUCLECTIDE SEQUENC: MEDLINE=20531754; Parrish.Novak J., Gross J.A., Johnstell Burkhead S., Heipe Conklin D., Presne. Mudri S., Clegg C. Raymond F., Ching; Maurer M., Kaushan "Interleukin 21 an regulation of lympj Nature 408:57-63(2) [2] NUCLECTIDE SEQUENC MEDLINE=20481926; Ozaki K., Kikly K. "Cloning of a type receptor beta chai:	HUMAN ; Q96H -2001, -2006, eukin- or). L21R; L21R; L21R;	2211.5 218.5 218.5 218.5 218.5 218.5 213.5 213.5 213.5 211.5 208.5
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Blakesley R.W., Jouchman J.W., Green E.
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EMBL; AF269133; AAG23419.1; -; m
EMBL; AY358826; AAQ89185.1; -; m
EMBL; AY064474; AAL39168.1; -; m
EMBL; BC004348; AAH04348.1; -; m
EMBL; BC007946; AAH07946.2; -; m
EMBL; BC007945; AAH07946.2; -; m
MIN; 605383; gene.

MIN; 605383; gene.

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0001532; F:interleukin-21 receptor activity

GO; GO:0030101; P:natural killer cell activation;

InterPro; IPR003961; FN_III.

InterPro; IPR003951; Hempt ropt S_F1.

PROSITE; PS50853; FN3; FALSE_NEG.

PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                   Ensembl; ENSG00000103522;
H-InvDB; HIX0012913; -.
HGNC; HGNC:6006; IL21R.
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Protein Sci. 13:2819-2824(2004).
-!- FUNCTION: This is a receptor for interleukin-21.
-!- SUBUNIT: Heterodimer with the common gamma chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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The box 1 motif is required for JAK interaction and
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or; Signal; Transmembrane
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                                                                   SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
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                                                                                                                                                LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS
                                                                                                                                                                                  RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
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         PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS
                                AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
                                           AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
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G -> S (in dbSNP:3093386).

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G -> R (in Ref. 2).

G -> R (in Ref. 2).
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RESULT 2
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ID IL21R MOUSE S
AC Q9UHX3; Q9ESM1;
DT 02-MAY-2002, int

STANDARD;

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integrated into

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Gross J.A., Johnston J., Melson A., Hammond A., Sprecher C., Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shinta F., Bort S., Hambly K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Poster D., "Interleukin 21 and its receptor are involved in NK cell expansion an regulation of lymphocyte function."; Nature 408:57-63(2000).
               Copyrighted Distributed
                                                                                                                                                                                                                                                         Submitted (JAN-2002) to -!- FUNCTION: This is a -!- SUBUNIT: Heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finne Dagdigian C., Lowe L., Wood C.R., Young D.A., Collins M "Chromosome 16p12 encodes a biologically active IL-2Rb receptor with lymphoid restricted expression."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997; Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.; "Cloning of a type I cytokine receptor most related to the IL-receptor beta chain."; Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
                                                                                                                                                                                                                                                           "Mus musculus interleukin 21 receptor gene Il21r mRNA.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is a receptor for interleukin-21.
-!- SUBUNIT: Heterodimer with the common gamma chain. As
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"A novel cytokine receptor NR8 is
polymorphism in Balb/c mouse.";
Submitted (SEP-2000) to the EMBL/G
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TISSUE S
                                                                                                                                                                       Most highly DOMAIN: The
                                                                                                                                                                                                                                SUBCELLULAR LOCATION:
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SIMILARITY: Contains 1 fibronectin type-III domain.
                                                                                                activation.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                    Teuscher
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                                                                                                                                                                                                  SPECIFICITY: Selectively expressed in
                                                                                                                                                     ghly expressed in thymus and spleen.
The WSXWS motif appears to be necessary for and thereby efficient intracellular transpo
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                                                                                                                            receptor binding
The box 1 motif :
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                                        the
AAG29347.1;
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                           the
                                          UniProt
                                                                                                                                                                                                                                                                                                                                [MRNA].
rTe, C57BL/6J, NOD/LtJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [MRNA].
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                           Creative Commons
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                                       Consortium,
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                                                                                                 type I
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                                                                                                                                                                                                                                                                                                                                  SJL/J; TISSUE=Spleen;
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DR EMBL; AF259134; AAG23420.1; -; mRNÅ.

DR EMBL; AF279436; AAF86350.1; -; mRNA.

DR EMBL; AF477982; AAL82632.1; -; mRNA.

DR EMBL; AF477982; AAL82632.1; -; mRNA.

DR EMBL; AF477983; AAL82633.1; -; mRNA.

DR EMBL; AF477984; AAL82635.1; -; mRNA.

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LLLVTDPAFLSCGCVSGSGLRLGGSPGSLLDRLRLSFAKEGDWTADPTWRTGSPGGGSES
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                    RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Balley T.L., Ambesi-Impiombato A., Apweiler R., Akuraliya R.N., Bailey T.L., RA Manbal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA Chowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Rei Pietcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Ra Pietcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Ra Georgii-Hemming P., Gingeres T.R., Golobori T., Green R.E., RA Georgii-Hemming P., Gingeres T.R., Golobori T., Green R.E., RA Kutchhari T.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu J., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu J., Lareau L.F., Lazarevic D., Lipovich L., Liu J., RA Kutano H., Mateuzawa S., Miki H., Mignone F., Miyake S., Morris K., RA Mottagui-Tabar S., Mulder N., Nakano N., Nakarchi H., Ng P., RA Mottagui-Tabar S., Mulder N., Nakano N., Nakarchi H., Ng P., Pavesi G., Pesole G., Pasotaki Y., Salzberg S.L., Sandelin A., Schneider C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Salzberg S.L., Sandelin A., Schneider C., RA Robet B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Ra Schibata Y., Shimada K., Sultana R., Takenaka Y., Taki K., Yan Immeriah K., Tang S.L., Tang S., Taylor M.S., Tegorer J., Teichmann S.A., Ra Yamanishi H., Zabarovsky E., Zhu, Shimata R., Takenaka Y., Taki K., Ra Yamanishi H., Zabarovsky E., Zhu, Shimata K., Mita J., Nakawa T., Nishiga S., Katatayama M., Suzuki M., Aoki J., Arakwa T., Pavesi G., Shibata K., Shiraki T., Suzuki S., Nakawa J., Pavesi G., Shibata K., Shiraki T., Suzuki S., Pavesi G., Shibata K., Shiraki T., Suzuki S., Pavesi G., Shibata K., Shiraki T., Suzuki S., Pavesi G., Shibata 
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Euarcho
Muroidea; Muridae; Murinae;
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Q3TAI3;
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"High-efficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cy version 6.
cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303:19-44(1999).
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RX MEDLINE-22354683; Pubmed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Schriml L.M., Kanagin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanagin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Gorbani L.E.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magdott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magdott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reeple C.A., Secou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang T., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Mayashizaki Y.,
RA Mayashiz
                                                                                                                                                                                                                                                                  RC STRAINS. TISSUE-Activated spleen;

RC MEDLINE-2108560; PubMedail217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

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RA Asaota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Baldarelli R., Barsh G.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Nordone P., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Saaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

PA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashiraki Y., Storch K., Fletcher C., Wilming L.,

RA Hayashirak
NUCLEOTIDE SEQUENCE.
STRAIN=NOD; TISSUE=Activated spleen;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genome Exploration Research Group, and Genome Scienc (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome.";
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                                                                                                                                                                                          Nature
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PubMed=16141073; DOI=10.1126/science.1112009
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                                                                                                                                                                                          409:685-690(2001).
                                                                                                                                                                                                                        annotation
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Matches 340
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-!- DOMAIN: The WSXWS motif appears to be necessary for proper prot folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tsahiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001792; Acylphosphatase.
InterPro; IPR003531; Hempt_rcpt_S_F1.
PRINTS; PR00112; ACYLPHPHTASE.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MGI:1890475; Il21r.
GO:0003998; F:acylphosphatase activity; RCA.
GO:0004907; F:interleukin receptor activity; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
SLELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFW----PTAQ
                                                                                                                        LLLLVIVFIPAFWSLKTHPLWRLWKKIWA-VPSPERFFMPLYKGCSGDFKKWVGAPFTGS
                                                                                                                                                                                                                                  RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                                                                                                                                                      APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                                                                                                                                                                                                                                                                                                      QETFCSLHRSGHNTTHIWYTCHMRLSQFLSDEVFIVNVTDQSGNNSQECGSFVLAESIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                                                                                                                                                                                                                                                                                         APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKLQYELQYRNLRDPYAVRPVTKLISVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                                                                                               RNVSLLPEEFHKDSSYQLQVRAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPHMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPRGPVAALLLLILHGAWSCLDLTCYTDYLWTITCVLETRSPNPSILSLTWQDEYEELQD
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Carninci P., Fukuda S., Hashizume W., Hayashida
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                                                                                        VFMGLKIHLPWRLWKKIWAPVPTPESFFQPLYREHSGNFKKWVNTPFTAS
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62.7%;
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49; Mismatches
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Attribution-NoDerivs License
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MEDLINE=22354683; PubMed=12466651; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kon
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PubMed=16141073; DOI=10.1126/science.1112009;
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MEDILNE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;

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                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                 MGI; MGI:1890475; Il21r.
GO; GO:0003998; F:acylphosphatase activity;
GO; GO:0004907; F:interleukin receptor activ
InterPro; IPR001792; Acylphosphatase.
InterPro; IPR003531; Hempt_rcpt_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
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"Functional
                                                                                                                                                                                                                                                                   Wynshaw-Boris A., Yoshida K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation (By similarity).
                                                                                                                                                                                340;
                                                                                                                                                                                                                                                                                                                                                                            AK150824; BAE29886.1; -;
                                                           61
                                                                                                                                                                                                Similarity
                                                                                                                                               WPRGWAAPLILLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKLQYELQYRNLRDPYAVRPVTKLISVDS
                            APPFNVTVTESGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                      EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                      MPRGPVAALLLLILHGAWSCLDLTCYTDYLWTITCVLETRRPNPSILSLTWQDEYEELQD
                                                                                                                                                                                                                                                          Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                            529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L/6J; TISSUE=Bone marrow; Carninci P., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                            58424 MW; 37524F07EB8C0967 CRC64;
                                                                                                                                                                                              58.6%;
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                                                                                                                                                                                  48;
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                                                           TCHMRLSQFLSDEVFIVNVI
                                                                                                                                                                                  Pred. No. 2.30
B; Mismatches
                                                                                                                                                                                                           Score 1734.5;
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                                                                                                                                                                                                                                                                                                                                                                              mRNA.
                                                                                                                                                                                                No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                        see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for JAK interaction
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                                                                                                                                                                                                                                                                                                                                                RCA.
                                                                                                                                                                                                            DB 2; Length
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                                                              QECGSFVLAES:
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow R.H., Scheefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Goulellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Robesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Philing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Scheun B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
      TISSUE=Thymus;
NIH MGC Project;
Submitted (FEB-20
-!- DOMAIN: The W
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15-MAR-2005, sequence version 1.
07-FEB-2006, entry version 9.
Interleukin 21 receptor (Predicted).
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Q5EBB1;
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      (FEB-2005) to the N: The WSXWS motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                         U.S.A.
EMBL/GenBank/DDBJ databases. appears to be necessary for proper
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Best Local Sim:
Matches 341;
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GO; GO:000.6021; C:integral to membrane;
GO; GO:0004872; F:receptor activity; IEX
InterPro; IPR003531; Hempt_rcpt_S_F1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNI
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Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transmembrane.
SEQUENCE 521 AA; 5743
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                                                                                                                                                                                                                                                                                                                                                                                                          MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
                                                                                                                                                                                                                                             APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                                                                                                                                                                                                                            SPLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS
                                               VTDPAFLSCGCVSGSGLRLGGSPGSLLDRLRLSFAKEGDWTAGPPWRTGSLEGGSESEAG
                                                                                                              GSAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLL
                                                                                                                                               SVELGPQSP----TTSV--LHLSLYPAKGKKFLGPLGLEEQLECDGMSGPGH----KCQG
                                                                                                                                                                                              LLLAVLILVLVFMGLKNHLPWRLCKKIWAPVPTPESFFQPLYREHSGNFKKWVNTPFTAS
                                                                                                                                                                                                           LLLLVIVFIPAFWSLKTHPLWRLWKKIWA-VPSPERFFWPLYKGCSGDFKKWVGAPFTGS
                                                                                                                                                                                                                                                                                                                                                         EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                                                                                                                                                                                                                                                                                                                                              MPRGLAAPLLLLILHGGWSCLDLTCYTDYLWTITCVLETWSPNPSILSLTWQDEYEELQD
SP-PGLDMDTFDSGFAGSDCGSPVET----DEGPPRSYLRQWVVRTPPPVDSGAQNS
                                                                     DAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAG
                                                                                              VSAYSEERDRPYGLVSIDTVTVGDAEGLGAWPFSCEDDGYPALNLDAVRESGPNGEDLLL
                                                                                                                                                                      SLELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSG
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RESULT 6
Q3TA82 MOUSE
ID Q3TA82 MOUSE PRELIMINARY; PRT; 292 AA.
AC Q3TA82;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Activated spleen cDNA, RIKEN full-length enriched lib clone:F830031M06 product:Interleukin 21 receptor, ful sequence. (Fragment).
DE sequence. (Fragment).
GN Name=1121r;
OS Mus musculus (Mouse).
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodenti OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognal Muroidea; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Sciurognathi;

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RC STRAIN=NOD, TISSUEActivated spleen,
RX PubMed=16141072; DOT=10.1126/science.1112014;
RX Carninci P., Kasukawa T., Katayama S., Goodh J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batealov S., Forrest A.R., Zavolan M.,
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RA Davis M.J., Wilming L.G., Addinis V., Allen J.E.,
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RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dallymple B.P., de Bono B., Della Gatta G.,
RA Crowe M.L., Dalla E., Dallymple B.P., de Bono B., Della Gatta G.,
RA Fletcher C.F., Fukushima T., Furuno M., Fukki S., Gariboldi M.,
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RA Kurochkin I. V., Lazeau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Kitano H., Mateuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Nottengui-Tabar S., Muder N., Nakanon N., Nakauchi H., Ng P.,
RA Natsaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
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RA Tangari M., Watsaki K., Watsaki T., Sasaki D., Arakawa T.,
RA Hayla M., Sasaki M., Ra Kana K., Shiva H., Nakano K.,
          STRAINNOD; TISSUE-Activated spleen;

X MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266;

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A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.

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A Baldarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

A Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins

A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

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A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN-NOD; TISSUE-Activated spleen;
PubMed=16141073; DOI=10.1126/science.1112009;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
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NUCLEOTIDE SEQUENCE.
STRAIN=NOD; TISSUE=Activated spleen;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The transcriptional landscape of Science 309:1559-1563(2005).
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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.ency full-length cDNA cloning.";
mol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mammalian
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                                                     Jarvis E.D.,
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Gojobori T.
                                                                                                                           Cousins
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RC STRAIN-NOD; TISSUE-Activated spleen;
RX MEDLINE-2108560; pubMed=1121785; DOI=10.1038/3505500;
RX MEDLINE-2108560; pubMed=1121785; DOI=10.1038/3505500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
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RA Alzawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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AN Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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Birney E., Hayashizaki Y.,
Tanalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                         STRAIN=NOD, TISSUE=Activated spleen;
MEDLINE=20530913; PubMed=11078861; DOI=10.1101/gr.152600;
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sequencing pipeline with 384 multicapillary sequencer.";
Cenome Res. 10:1757-1771(2000).
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STRAIN=NOD; TISSUB-Activated spleen;
STRAIN=NOD; TISSUB-Activated spleen;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
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"Normalization and subtraction of rapid discovery of
STRAIN=NOD; TISSUE=Activated spleen; Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninon Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasi Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watal
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420:563-573(2002).
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                                            RP NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.24260389;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038;

RX MEDLINE=22388257; PubM
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Nus musculus (Mouse).
Rukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognat
Muroidea; Muridae; Murinae; Mus.
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Q6PEU8;
05-JUL-2004, integrated into U
05-JUL-2004, sequence version
07-FEB-2006, entry version 16
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GO:0004907; F:interleukin receptor activity;
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оv R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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A6_CHICK
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Q5F4A6;
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Eukaryota; Metazoa; Chore
Archosauria: Avec.
                                               NUCLEOTIDE SEQUENCE.
STRAIN=CB; TISSUE=Bursa;
Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim Caldwell R.B., Kierzek A.M., Kostoveka D., Koter Fiedler P., Kutter S., Blagodatski A., Kostoveka D., Koter Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length cDNAs from chicken bursal lymphocytes to facil
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GO; GO:0004907; F:interleukin receptor activity;
InterPro; IPR003531; Hempt rcpt S F1.
PROSITE; PS01355; HEMATOPO_REC_S F1; 1.
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Ensembl; ENSMUSG00000030745; Mus musculus.
MGI; MGI:1890475; Il21r.
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                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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DOWAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).

BOMAIN: The box 1 motif is required for JAK interaction and/or actives for the form the form of the following 
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Best Local S
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IL2RB MACFA
Q38J85;
10-JAN-2006, i
                                                                   22-NOV-2005, sequence version 1.
07-FEB-2006, entry version 4.
Interleukin-2 receptor beta chain
(High affinity IL-2 receptor beta
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HYDothetical protein; Immunoglobulin domain; Repeat; T
SEQUENCE 590 AA; 66332 MW; 369CA086F9A95867 CRC64;
             Eukaryota; Metazoa; Chordata; Craniata; Vertebr
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                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involved in receptor mediated endocytosis and transduces the mitogenic signals of IL2 (By similarity).

SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R exists in 3 different forms: a high affinity dimer, an intermediate affinity monomer (beta chain), and a low affinity monomer (alpha chain). The high and intermediate affinity forms also associate with a gamma chain (By similarity).

SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
SIMILARITY: Contains 1 fibronectin type-III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activation SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      folding and thereby efficient intracellular transport as surface receptor binding (By similarity).

DOMAIN: The box 1 motif is required for JAK interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (By DOMAIN: The
                                              217
                                                                        168
  269
                                                                                              157
                                                                                                                                              101
                                                                                                                                                                      53
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                                                                                                                                                                                                                                          ហ
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       υY
                                                                                                                                           QSGN--YSQECGSFLLAESIKPAPPFNVTVTF--SGQYNISWRSDYEDPAFYMLKGKLQY
                                                                                                                                                                                           ELKDEATSCSLH----RSAHNAT-----HATYTCHM-----DVFHFMADDIFSVNITD
                                                                                                                                                                                                                                          WAAPLLLLLQGGW-----
  A. - VPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGPWSPEVPSTLEVYSCHPPRSPA
                        WSQPLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGP-----WLKKVL
                                       WSDPVIFQTQSEELKEG---WNPHLLLLLLLLVIVFIPAFWSL----KTHPLWRLW-KKIW
                                                                         EARTLS PGHTWEEAP - - -
                                                                                              ELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSE
                                                                                                                       REGVRWRMMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWKI---SQASHYFERHLEF
                                                                                                                                                                      ALQD-
                                                                                                                                                                                                                    WCLPLLILLPLATSSASAAVNGTSRFTCFYNSRANISCV---WS-----
                                                                                                                                                                                                                                                                                                                                                   27
241
266
266
131
220
278
29
243
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                      -TSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGTPDSQKLTAVDIVTLRVMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
WSXWS motif appears to be necessary for proper protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belongs to the type I cytokine receptor
                                                                                                                                                                                                                                                                                                              240
555
529
229
2824
29
29
43
43
449
149
149
61224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [MRNA].
                                                                                                                                                                                                                                                                              26.4%;
                                                                                                                                                                                                                                                                                        9.9%;
                                                                                                                                                                                                                                                                                                                   Œ,
                                                                         LMTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEF--TTWSP
                                                                                                                                                                                                                                                                                                                                                  Box 1 motif.
N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
                                                                                                                                                                                                                                                                  Score 294; DB 1;
Pred. No. 2.4e-12;
3; Mismatches 200
                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                               SMXSM
                                                                                                                                                                                                                                                                                                                                                                                                                             Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential)
                                                                                                                                                                                                                                          GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE
                                                                                                                                                                                                                                                                                                                   SCEAEC1A802A1D50
                                                                                                                                                                                                                                                                                                                                                                                                              motif
                                                                                                                                                                                                                                                                                                                                                                                                                          type-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta subunit
                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
                                                                                                                                                                                                                                                                    114;
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                                                                                                                         167
                                                                                                                                                156
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RESULT 10
QGUAP3 TETING
QGUAP5
ID QGUAP5;
AC QGUAP5;
AC QGUAP5;
AC QGUAP5;
DT 05-JUL-2004, integrated into Unip
O5-JUL-2004, sequence version 10.
DT 05-JUL-2004, sequence version 10.
DT 07-PEB-2006, entry version 10.
DC Class I helical cytokine receptor
GN NGBL_TAXID=9983;
RN 10.
CC Actinopterygii; Neopterygii; Tell
OC Actinopterygii; Neopterygii; Tell
OC Actinopterygii; Neopterygii; Tell
OC Actinopterygii; Neopterygii; Tell
OC Tetradontoidea; Tetraodontidae;
RN NUCLEOTIDE SEQUENCE.
RN NUCLEOTIDE SEQUENCE.
RN NICLEOTIDE SEQUENCE
RN NICLEOTIDE
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Best Local S
Matches 143
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A nithouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
A Cruaud C., Lardier G., Chapple C., McKarnan K.J., McEwan P., Bosak S.,
A Parra G., Lardier G., Chapple C., McKarnan K.J., McEwan P., Bosak S.,
A Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
A Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Tenome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class I helical cytokine receptor Name=CRFA13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; AY374485; Tetraodon nigroviridis. GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY374485; AAR25676.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15496914; DOI=10.1038/nature03025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
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                                                                                                                                                                                                                                                                      143;
   68
                                                              63
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LGGP-----LGSLLDRLKPPLAD--GEDWAGGLPWGGRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERDKVTQL----LLQQDKVPEPS----SLSSNRSLTSCFTNQGYFFFHLPDALEIEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRLQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG
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                                                                     TSCSLHRSAHNATHATYTCHMDVFHFMA------DDIFSVN-----ITDQSGN--YSQ 107
                                                                                                                                                                                                   LLLLLQGGWGCPDLV-----CYTDYLQTVIC-ILEMWNLHPSTLTLTWQDQYEELKDEA
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                        -CAAVVSRCNVTCSTDYNVSLNCSCAEAVQTRSVFLHVKCSDEGIDVED--
                                                                                                                                                                                                                                                                      9.7%; Score 286; DB 2;
24.4%; Pred. No. 8.1e-12;
tive 76; Mismatches 203
   SCEVKPFQSWCVMSPESLEDVLSVSTMCDARATDGDGAPIDSS 110
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                                                                                                                                                                                                                                                                                                                                                                                                           E058418483A5DF0B CRC64;
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                                                                                                                                                                                                                                                                      203;
                                                                                                                                                                                                                                                                                                                                        Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Segurens B.,
                                                                                                                                                                                                                                                                         164;
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  RESULT 11
IL2RB_PANTR
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                                                                                                                                    RA Chen S., Yu I.;

RA Chen S., Yu I.;

RA Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.

RC :- FUNCTION: Receptor for interleukin-2. This beta subunit is completed in receptor mediated endocytosis and transduces the involved in receptor mediated endocytosis and transduces the complete signals of II2 (By similarity).

RC :- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R componer (signals endiny monomer (beta chain), and a low affinity componer (signals chain). The high affinity dimer, an intermediate affinity forms componer (alpha chain). The high and intermediate affinity forms componer (alpha chain). The high and intermediate affinity forms componer (alpha chain). The high and intermediate affinity forms componer (alpha chain). The similarity) is similarity).

RC :- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane componer in the MSXMS motif appears to be necessary for proper protein componer protein componer protein componer componer by similarity).

RC :- DOMAIN: The WSXMS motif appears to be necessary for proper protein component componer by similarity).

CC :- DOMAIN: The box 1 motif is required for JAK interaction and/or component co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2006, integrated into UniProtKB/Swiss-Prot. 22-NOV-2005, sequence version 1. 07-FBB-2006, entry version 4. Interleukin-2 receptor beta chain precursor (IL-2 (High affinity IL-2 receptor beta subunit) (CD122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=IL2RB;
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SIMILARITY:
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IL2RB HUMAN STANDARD; PI P14784; P14784; Integrated into Uni 01-APR-1990, integrated into Uni 01-APR-1990, sequence version 1. 07-MAR-2006, entry version 78. Interleukin-2 receptor beta chai (p75) (High affinity IL-2 recept
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        RA Dunham I, Hunt A.R., Collins J.E., Brusklewich R. Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bardy C.P., Balkey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Durton J., Carder C., Catter N.P., Chen Y., Clark G.,
RA Burrill W.D., Dockree C., Doddworth S.J., Durbin R.M., Ellington A.G.,
RA Clayg S.M., Cobley V.E., Cobal C.G., Collier R.E., Connor R.,
RA Clayd S.M., Cobley V.E., Doddworth S.J., Durbin R.M., Ellington A.G.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Morrimore B.J.,
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RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
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RA Martyn I.D., Malaren S., McMurray A.A., Milne S.A., Morrimore B.J.C.T.,
RA Mallians S.H., Plumb R.W., Rameay H., Ramesy Y., Rogers L., Ross M.T.,
RA Millians S.H., Plumb R.W., Rameay H., Ramsey Y., Rogers L., Ross M.T.,
RA Millians L., Williams S.A., Williamson H., Wilner T.E., Williang L.,
RA Willians L., Williams S.A., Williamson H., Wilner T.E., Williang S.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Mang O., Wang Y., Wang Z., White J., Bentley D.R., Benk S., Do A., Do T.,
RA Mang O., Wang Y., Wang Z., White J., Williang D., Wu H., Yao Z.,
RA Mang O., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
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RA Mang O., Wang Y., Wang Z., White J., Wandlashi H., Salotn S.,
RA Mang O., Wang S., Malkhin, Malashi H., Salotn S.,
RA Mang O., Wang S., Shakh T., Karahashi H., Salota S.,
RA Mang O., Wang S., Shakh T., Karahashi H., Salota S.,
RA Ma
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Miyasaka M., Taniguchi T.;
"Interleukin-2 receptor beta chain gene:
forms by cloned human alpha and beta chai
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MEDLINE=89242117; PubMed=2785715;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10591208;
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Mallya M., Mokrab
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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"Generation and initial analysis of more than 15,000 full-length human for the proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
EMBL; M26062; AAA59143.1; -; mRNA.

EMBL; CR456506; CRG30392.1; -; mRNA.

EMBL; AF517934; AAM54040.1; -; Genomic_DNA.

EMBL; AL022314; CAA18444.1; -; Genomic_DNA.

EMBL; BC025691; AAH25691.1; -; mRNA.

PIR; A30342; A30342.

PDB; 11LM; Model; B=31-230.

PDB; 11LM; Model; B=31-230.

PDB; 11LN; Model; B=31-230.

PDB; 2B51; X-ray; B=27-240.

Ensembl; ENSG00000100385; HOmo sapiens.

H-InvDB; HIX0016437; -
HGNC; HGNC:6009; IL2RB.

MIM; 146710; gene.

GO; GO:0005887; C::Integral to plasma membrane;
GO; GO:0005887; C::Integral to plasma membrane;
GO; GO:0006461; F::protein complex assembly; TAS.

GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure 2:839-851(1994).

Structure 2:839-851(1994).

-I- FUNCTION: Receptor for interleukin-2. This beta subunit is involved in receptor mediated endocytosis and transduces the mitogenic signals of IL2.

-I- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R exists in 3 different forms: a high affinity dimer, an intermediate affinity monomer (beta chain), and a low affinity monomer (alpha chain). The high and intermediate affinity forms also associate with a gamma chain.
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3D-STRUCTURE MODELING OF 31-230.
MEDLINE=95111955; PubMed=7529123;
Bamborough P., Hedgecock C.J., Richards W.
                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
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; 146710; gene.
; 146710; gene.
GO:0005887; C:integral to plasma membrane; TAS.
GO:0005886; C:plasma membrane; TAS.
GO:0004911; F:interleukin-2 receptor activity;
GO:0006461; P:protein complex assembly; TAS.
GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface
DOMAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
SIMILARITY: Contains 1 fibronectin
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SIMILARITY:
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The box 1 motif is
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                                                     ELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSE
                                                                                   QSGNYSQECG--SFLLAESIKPAPPFNVTVTF--SGQYNISWRSDYEDPAFYMLKGKLQY
                                                                                                                                      WAAPLLLLL--LQGGW-----
A--VPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGPWSPEVPSTLEVYSCHPPRSPA
              WSQPLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGP
                     WSDPVIFQTQSEELKEG---WNPHLLLLLLLVIVFIPAFWSL----KTHPLWRLW-KKIW
                                          EARTLS PGHTWEEAP --- LLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEF -- TTWSP
                                                                      REGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEI----SQASHYFERHLEF
                                                                                                 ALQD--TSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLC
                                                                                                                ELKDEATSCSLH----
                                                                                                                              WRLPLLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS------
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551
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75; Mismatches
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By similarity.
S -> F (in dbSNP:3218273).
                                                                                                                                                                                                                                                                                                                                                                             N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                                                                               SMXSM
                                                                                                                                                                                                                                                                                                                                                                                           N-linked
                                                                                                                                                                                                                                                                                                                                                                                                  N-linked
                                                                                                                                                                                                                                                                                                                                                                                                         Box 1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular Potential.
                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_019998
                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_021994.
D -> E (in dbSNP:228942)
                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-2 receptor beta
/FTId=PRO_0000010878.
                                                                                                                                         -GCPDLVCYTDYLQTVIÇILEMWNLHPSTLTLTWQDQYE
                                                                                                                                                                                                                                                                                                                                                                                                                moti
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    Polymorphism; Receptor; Signal;

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1 (GlcNAC. ..)
1 (GlcNAC. ..)
1 (GlcNAC. ..)
                                                                                                                                                                DB 1;
.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
type-III.
                                                                                                                                                                       Length
                                                                                                                                                          Indels 116;
                                                                                                                                                                                                                                                                                                                                                                             (Potential). (Potential). (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain.
              -WLKKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; DQ273166; ABB77800.1; -; mRNA.
GQ; GQ:0004872; F:receptor activity; IEA.
Membrane; Receptor; Repeat; Transmembrane.
SEQUENCE 509 AA; 57872 MW; ADA014E174FCD380 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paffett-Lugassy N.N., Yang C., Paw B., Leschinsky I., Barut B.,
Bahary N., Caro J., Handin R., Zon L.;
"Functional conservation of epo-epor signaling in zebrafish.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- DOWAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Žebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                               194
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                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
PWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESD-----GVPKPSFWPTAQNSG 359
                                                       SMTVILSHHKF--LLKKLWPDIPTPEHKFPGLFTVYKGDFKEWM-SQNSGSMWARSVQM-
                                                                                                                                                               SSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLLLLLLLVIVFIPAFW
                                                                                                                                                                                                  NVSWL----PPAVKYIDDSLIYEVRY-----AVEDSHMGKVEETKASTMLVLRGLQPD
                                                                                                                                                                                                                                   NISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLE-FRKD 193
                                                                                                                                                                                                                                                                                                                                                                             DLVCYTDYLQTVICILEM----WNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHAT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERDKYTQL----LLQQDKYPEPA----SLSSNHSLTSCFTNQGYFFFHLPDALEIEA--
                                                                                          S----LKTHPLWRLWKKIWA-VPSPERFFMPLYKGCSGDFKKWVGAPFTGS----SLELG
                                                                                                                            TRYKVWVRVKP-DGVSYKGYWSSWTSPVIAVT----PPGSMDPLIVLLVVFIILILCLL
                                                                                                                                                                                                                                                                                                       YTCHM-DVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFS---GQY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLLGGPSPPSTAPGGSGAGEERMPPSLQERVPRDW-DPQPLGPPTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-LGGP-----LGSLLDRLKPPLAD--GEDWAGGLPWGGRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCNTPDPSKFFSQLSSEHGGDVQKWLSSPFPSSSFSPGGLAPEI-SPLEV-----L
                                                                                                                                                                                                                                                                      FFCKLPKALFFTSLDVQVLRDGQMLYNRSLNVENILLTD-----PPRNVTVWSSGKEGQL 152
                                                                                                                                                                                                                                                                                                                                            DIKCFVEGKKDFTCFWEKEDGTNYSQDNYTFTYTYMNENKMDCAVS-SLFLLSSN--RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRLQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSG-ED---DAYCTFPSRDDLLLFSP
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                70; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 261; DB 2;
Pred. No. 4.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 509;
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                                                        311
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                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                              Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane; Receptor; SEQUENCE 890 AA;
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50853; FN3; 3.
PROSITE; PS50853; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 3.
PIRSF; PIRSF001956; IL3R_beta_c; 1.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004907; F:interleukin receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0019221; P:cytokine and chemokine mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U94688; AAC7
HSSP; P32927; 1GH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999, integrated into UniProtKB/TrEMBL 01-MAY-1999, sequence version 1. 07-FBB-2006, entry version 26. Interleukin-5 receptor beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Z1A0_CAVPO
Q9Z1A0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003531; InterPro; IPR011365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002996; Cytkn_rcpt_B/G.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312
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  289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U94688; AAC77520.1; -; mRNA.
                                                                                                                                                             N
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                          PRGWAAPLLLLLQGGWGCP-DLVCYTDYLQTVICILEMWNLHPSTLTLTW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSAGTSSINASHSDLGSLRQSSASGRLSSQ-----SSFED--PNHPWPPKGPGYAYMAVA
  EQECPQVQKEELHDIYTRHSCQI-RVSNPRPHSQYT
                                              -----QDQYEELKDEAT--SCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSG-
                                                                                                     PSQWSPEVSWSSQPGDQAQPQNLQCVFDGAHTLSCSWEVRSQVTSSVSFGLFYRSSLDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPLAGLDMD 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSAYSEERDRPYGLVSIDT-VTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YTEELPSPLEVLS-----EVSLSPLDERKLVRDEDQRSDSGLTEPPHWLMEQLRA
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                8.5%; 50
22.7%; Pred
379
73;
                                                                                                                                                                                                                                                                                                                       Transmembrane.
96579 MW; D43FB1CA88525536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hempt_rcpt_S_F1.
IL3_rcpt_beta.
                                                                                                                                                                                                              Score 250; DB 2;
Pred. No. 6.2e-09;
3; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                Length 890;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                    220;
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        VIVRPRNGE
                                                                                                                                                                                                                 Gaps
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"Molecular cloning of cDNAs for the rat interle
and beta chain genes: differentially regulated
response to mitogenic stimulation.";
Eur. J. Immunol. 21:2133-2138(1991).
-i- FUNCTION: Receptor for interleukin-2. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p26896;
01-AUG-1992, integrated into Unibr
01-AUG-1992, sequence version 1.
07-MAR-2006, entry version 51.
Interleukin-2 receptor beta chain
(High affinity IL-2 receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL2RB
                                                             -
                                                                                                                                                                                                                                                                      <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91364784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Il2rb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                              protein.
DOMAIN:
folding
                                                                                                          FUNCTION: Receptor for interleukin-2. This beta subunit is involved in receptor mediated endocytosis and transduces the mitogenic signals of IL2.
SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R exists in 3 different forms: a high affinity dimer, an intermediate affinity monomer (beta chain), and a low affinity monomer (alpha chain). The high and intermediate affinity forms also associate with a gamma chain.
SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461
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The WSXWS motif appears to and thereby efficient intra receptor binding.
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PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

Glycoprotein; Membrane; Receptor; Signal; Transmembrane SIGNAL 1 26
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By similarity.
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Search Job tim	Ъ	ş	Db	Ş	ď
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Perfect score:
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1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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                                                   US-09-923-246-115
US-10-295-723-115
US-10-295-723-115
US-10-295-761A-2
US-09-825-561A-6
US-09-949-016-11544
US-09-949-016-11544
US-09-825-561A-65
US-09-404-641-85
US-09-825-561A-12
US-09-825-561A-12
US-09-825-561A-16
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Sequence 2, Appli
Sequence 115, App
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Sequence 2, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 12, Appli
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                                                                                                                               Matches 538;
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7.5	7.5	7.8	8.4	8.4	9.4	9.4	9.4	9.4	9.4	22.9	22.9	22.9	28.5	37.2	38.4	40.4	40.5	40.5
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US-08-456-489B-7	US-08-164-614A-7	US-09-949-016-8560	5198359-4	5449756-4	US-09-949-002-537	5449756-2	5198359-2	US-09-949-002-308	US-09-194-145-2	US-10-243-072-70	US-10-414-186-70	US-09-404-641-70	US-09-825-561A-73	US-09-825-561A-69	US-09-825-561A-71	US-09-825-561A-6	US-10-243-072-51	US-09-825-561A-30
Sequence	Sequence	Sequence	Patent No.	Patent No.	Sequence	Patent No.	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
7, Appli	7, Appli	8560, Ap	. 5198359	. 5449756	537, App	. 5449756	•	308, App	2, Appli	70, Appl		70, Appl				6, Appli	51, Appl	30, Appl

ALIGNMENTS

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RESULT 1
US-09-040-005-2
TOPOLOGY: linear; MOLECULE TYPE: protein US-09-040-005-2
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                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION NUMBER: US/09/040,005
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15320
                                                                                                                                    TELEFAX: 617-876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Donaldson, Debra
APPLICANT: Unger, Michelle
TITLE OF INVENTION: MU-1 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                        STRANDEDNESS:
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CITY: Cambridge
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617-876-5851
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100.0%; ilarity 100.0%; Conservative 0

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Score 2958; DB 2; Pred. No. 3.6e-267; Mismatches 0;

Length

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Gaps

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APPLICANT: Sprecher, Cindy A.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT FILLING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US/09/522,217
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILLING DATE: 1999-03-09
EARLIER FILLING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILLING DATE: 1999-03-11
EARLIER FILLING DATE: 1999-03-11
EARLIER FILLING DATE: 1999-07-01
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                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115
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US-09-522-217-115
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 115
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 115, App
Patent No. 630702
GENERAL INFORMATION
                                                          Query Match 100.0%; Score 2958; DB 2; Best Local Similarity 100.0%; Pred. No. 3.6e-267; Matches 538; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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 MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
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                                                                                                                                                 Query Match
Best Local Similarity
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538;

100.0%; Silarity 100.0%; F Conservative 0;

Score 2958; DB 2; Pred. No. 3.6e-267; Mismatches 0;

Length Indels

538; 0;

Gaps

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EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP

120 60 60

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Sequence 2, Application US/09404641

Sequence 2, Application US/09404641

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Conklin, Darrell C.

APPLICANT: Hammond, Angela K.

FILE REFERENCE: 98-55

CURRENT APPLICATION NUMBER: US/09/404,641

CURRENT FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 60/100,896

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 60/123,546

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,546

PRIOR RILING DATE: 1999-07-06

PRIOR RILING DATE: 1999-07-06

INMBER OF SEO ID NOS: 91

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 538

TYPE: PRT

ORGANISM: Homo sapiens
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US-09-404-641-2
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILLS OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
CURRENT APPLICATION NUMBER: US/09/923,246.
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER PILOR DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 538
TYDE: DET
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US-09-923-246-115
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                                                                                                                                         Matches
                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo
-09-923-246-115
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                    EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
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 EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
                                                                      MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
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                                                                                                                                  100.0%; Score 2958; DB 2; ilarity 100.0%; Pred. No. 3.6e-267; Conservative 0; Mismatches 0;
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; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo s
US-10-295-723-115
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CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
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APPLICANT: NO. 6686178ak, Julia E.
APPLICANT: Presenell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
Tane A.
                                                                 Query Match
Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 115
LENGTH: 538
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll
FILE REFERENCE: 99-16
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 MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD
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                                                                   100.0%; Score 2958; DB 2; ilarity 100.0%; Pred. No. 3.6e-267; Conservative 0; Mismatches 0;
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EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP

EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP

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APPLICANT: Presnell, Scott R.

APPLICANT: Conklin, Darrell C.

APPLICANT: No. 6692924ak, Julia E.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11

FILE REFERENCE: 98-55

CURRENT APPLICATION NUMBER: US/10/414,186

CURRENT FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: US/9/404,641

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/404,641

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/404,641

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/404,641

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/404,641

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09

PRIOR FILING DATE: EARLIER FILING DATE: US 60/
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; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo s
US-10-414-186-2
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                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 538; Conservative 0;
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                                                                                                                                                                                      Score 2958; DB 2;
Pred. No. 3.6e-267;
N. Mismatches 0;
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FILE REFERENCE: 00-22

CURRENT APPLICATION NUMBER: US/09/825,561A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/194,731

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/222,121

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FBSTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 538
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US-09-825-561A-2
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GENERAL INFORMATION:
                                                                                                                                                        Query Match
Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo
-09-825-561A-2
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
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                                                                                                                                                       100.0%; Score 2958; DB 2; ilarity 100.0%; Pred. No. 3.6e-267; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: PRESENT!], SCOTT R.
APPLICANT: CONKIIN, DARRELI C.
APPLICANT: No. 6803451ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKKINE RECEPTOR ZAPLHA11
FILE REFERENCE: 98-55C1
CURRENT APPLICATION NUMBER: US/10/243,072
CURRENT APPLICATION NUMBER: 09/628,127
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR APPLICATION NUMBER: US 09/404,641
PRIOR APPLICATION NUMBER: US 09/404,641
PRIOR APPLICATION NUMBER: US 09/404,641
PRIOR FILING DATE: 1999-09-23
SOFTWARE: PRIOR DATE: 1999-09-23
LENGTH: 538
TYPE: PRI
CORMISM: Homo sapiens
US-10-243-072-2
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US-10-243-072-2
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Patent No. 6803451
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APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: No. 6929932ak, Julia E.

APPLICANT: No. 6929932ak, Julia E.

APPLICANT: No. 6929932ak, Julia E.

TITLE OF INVENTION: ZALPHAI1 LIGAND ANTAGONISTS

FILE REFERENCE: 01-37

CURRENT APPLICATION NUMBER: US/10/282,622

CURRENT APPLICATION NUMBER: 60/337,586

PRIOR APPLICATION NUMBER: 60/337,586

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 538

TYPE: PAT

ORGANISM: Homo sapiens

US-10-282-622-16
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US-10-282-622-16
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GENERAL INCOMPATION:
GENERAL INCOMPATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-4-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 00/231,498
PRIOR APPLICATION NUMBER: 00/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEG ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 11544
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TYPE: PRT
ORGANISM: Human
S-09-949-016-11544
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Best Local Similarity
Matches 538; Conserv
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                                                                                SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
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APPLICANT: Sprecher, Cindy A.

APPLICANT: No. 6777539ak, Julia E.

APPLICANT: No. 6777539ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Presnell, Scott R.

APPLICANT: Nelson, Andrew J.

FILE REFERENCE: 00-22

CURRENT APPLICATION NUMBER: US/09/825,561A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/194,731

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 65

LENGTH: 568

TYPE: PRT

ORGANISM: homo sapiens
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US-09-825-561A-65
; Sequence 65, Application US/09825561A
parent No. 6777539
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Best Local Similarity 89.9%;
Matches 523; Conservative
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                                                                                                                                                            THPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGPWSPEVPSTLEV
                                                                                                                                                                                                              SWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSY 196
              GLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMDTFDSGFVG
                                                                                                                                                                                                                                                                                                                           ATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAE-----SRQYNI
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                                                                                                                                                                                                                                                                                                                                                                                              GLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMDTFDSGFVG
                                                  DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLDAGTTVLSCGCVSAGSP
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Pred. No. 5.6e-254;
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APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. 6576744ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
NUMBER: Estren for Windows Version 3 0
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Best Local Similarity
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LENGTH: 529
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             EAGSP-PGLDMDTFDSGFAGSDCGSPVET---
                                     EAGSPLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLROWVVIPPPLSSPGPQ
                                                               LLLVTDPAFLSCGCVSGSGLRLGGSPGSLLDRLRLSFAKEGDWTADPTWRTGSPGGGSES
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             -DEGPPRSYLRQWVVRTPPPVDSGAQ
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US-10-414-186-85
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US-10-414-186-85
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GENERAL INFORMATION:
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APPLICANT: Conklin, Darrell C.
APPLICANT: No. 6692924ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
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                EAGSPLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQ
                                                                      PLLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSES
                                                                                                    GOAVSAYSEERDRPYGLVSIDTVTVGDAEGLCVWPCSCEDDGYPAMNLDAGRESGPNSED
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Pred. No. 4.6e-153;
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DB 2;

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60/100,896

Indels Length

17;

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; TYPE: PRT
; ORGANISM: mus musculus
US-09-825-561A-12
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APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09825561A Patent No. 6777539
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Best Local !
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APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
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Local Similarity 62.7%;
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                  EAGSPLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQ 536
                                                                                                     PLLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSES 476
                                                                                                                                                                       NSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLED 416
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                                                                  LLLVTDPAFLSCGCVSGSGLRLGGSPGSLLDRLRLSFAKEGDWTADPTWRTGSPGGGSES
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; Pred. No. 4.6e-153;
49; Mismatches 136;
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RESULT 15
US-10-243-072-85
; Sequence 85, Applic
; Patent No. 6803451
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APPLICANT: CONKlin, Darrell C.
APPLICANT: No. 6803451ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAll
FILE REFERENCE: 98-5SC1
CURRENT APPLICATION NUMBER: US/10/243,072
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/628,127
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR APPLICATION NUMBER: US 09/404,641
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 85
LENGTH: 529
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TYPE: PRT
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                                     LILLVTDPAFLSCGCVSGSGLRLGGSPGSLLDRLRLSFAKEGDWTADPTWRTGSPGGGSES
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2: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US108_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US108_PUBCOMB.pep:*

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US-10-456-780-6

US-10-659-684-115

US-10-659-684-115

US-10-620-1694-4

US-10-872-087-2

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US-10-98-380-43

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	32, App	2, App1	6, Appl	4, Appl	10, App	8, Appli		45, App	12, App	•	2, App1	•	85, App	•				

ALIGNMENTS

Sequence 2, Application US/09965313 Patent No. US20020090680A1 GENERAL INFORMATION: APPLICANT: Hodge, Martin R. ITILE OF INVENTION: No. US20020090680A1el IL-9/IL-2 Receptor-Like Molecules TITLE OF INVENTION: and Uses Thereof FILE REFERENCE: 5800-17A CURRENT APPLICATION NUMBER: US/09/965,313 CURRENT FILING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: US 09/313,913 PRIOR PRIOR APPLICATION NUMBER: US 09/313,913 PRIOR FILING DATE: 1999-05-18 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 538 ; TYPE: PRT ; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like US-09-965-313-2 RESULT 1 US-09-965-313-2 Query Match Best Local Similarity Matches 538; Conserv 301 301 241 241 181 181 RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL 121 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS 361 61 61 EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP μ 1 MPRGWAAPLLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTUTWQDQYEELKD LLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP MPRGWAAPLILLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKD SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG 100.0%; Score 2958; DB 3; ilarity 100.0%; Pred. No. 2.8e-228; Conservative 0; Mismatches 0; 0; DB 3; Indels Length 0; Gaps 180 360 300 300 180 120 360 240 240 120 60

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FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

CURRENT FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

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APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Conald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond, Angela K.
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APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
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LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG 360
                                                                                                         LLLLVIVEIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS 300
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; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo s
US-09-825-561A-2
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PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
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APPLICANT: No. US20020137677A1ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Pessnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE REFILE REFERENCE: 00-22
FILE REFERENCE: 00-22
FURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT APPLICATION PROPERTY OF COLORS
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Similarity 100.0%;
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                                                        SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
                                                                                                                            LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
                                   SAYSEERDRPYGLVSIDTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPLLD
                                                                                                           LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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Pred. No. 2.8e-228;
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538

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GENERAL INFORMATION: Whitters, Matthew J
APPLICANT: Carter, Laura
APPLICANT: Collins, Mary
APPLICANT: Collins, Mary
APPLICANT: Collins, Mary
APPLICANT: Voung, Deborah A.
APPLICANT: Voung, Deborah A.
APPLICANT: Lowe, Leslie D.
APPLICANT: Unger, Michelle
TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
FILE REFERENCE: 22058-552CIP2
CURRENT APPLICATION NUMBER: US/09/972,218A
CURRENT APPLICATION NUMBER: 09/569384
PRIOR APPLICATION NUMBER: 09/569384
PRIOR APPLICATION NUMBER: 09/560766
PRIOR APPLICATION NUMBER: 09/560766
PRIOR APPLICATION NUMBER: US/6057128
PRIOR APPLICATION NUMBER: US/6057128
PRIOR APPLICATION NUMBER: US/6057128
PRIOR APPLICATION NUMBER: 09/560766
PRIOR APPLICATION NUMBER: 09/560766
PRIOR FILING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: US/6057128
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 2
LENGTH: 538
TYPE: DET
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; ORGANISM: Human
US-09-972-218A-2
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US-09-972-218A-2
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                         AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
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GENERAL INFORMATION:
APPLICANT: Donaldson, Debra et al.
FILE REFERENCE: G15320-B3
CURRENT APPLICATION NUMBER: US/10/264,634
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 09/040,005
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: 09/560,766
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/972,218
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/972,218
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/373,746
PRIOR APPLICATION NUMBER: 60/373,746
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATE 10 NOS: 45
SEQ ID NOS: 47
SEQ ID NOS: 48
SOFTWARE: PATE 10 NOS: 49
SOFTWARE: PATE 10 NUMBER: 10 NOS: 49
SOFTWARE: PATE 10 NUMBER: 10 NUMBER: 10 NUMBER: 10 NUMBER: 10 NUMBER: 10 NU
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US-10-264-634-2
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                                                                                                                                                                                                                                                                                                                                                                                     RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
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                              PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS 538
                                                                                                                        AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS 480
                                                                                               AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSESEAGS
                                                                                                                                                                                                                                                                                          LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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Gaps

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538

300

240

180

300

US-10-295-723-115

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Sequence 115, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, Ju
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
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APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-01
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Matches
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LENGTH: 538
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APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
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Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
Johnston, Janet V.
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                                                   LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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o. US20030125524A1
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Pred. No. 2.8e-228;
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RESULT 8 US-10-243-072-2

Sequence 2, Application US/10243072 Publication No. US20030148447A1 GENERAL INFORMATION:

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Sequence 16, Application US/10282622

Publication No. US20030134390A1

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. US20030134390A1ak, Julia E.
APPLICANT: No. US20030134390A1ak, Julia E.
APPLICANT: No. US20030134390A1ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS

FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR APPLICATION STATE 1003-11-05
NUMBER OF SEG ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0

SEG ID NO 16
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; TYPE: PRT
; ORGANISM: Homo s
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Best Local Similarity 100.0%;
Matches 538; Conservative 0,
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                    PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLROWVVIPPPLSSPGPQAS
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Pred. No. 2.8e-228;
; Mismatches 0;
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; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo &
US-10-243-072-2
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/628,127
PRIOR FILING DATE: 2000-07-28
PRIOR PRIOR PLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR PRIOR PRIOR DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 09/404,641
PRIOR PILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 92
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
         RESULT 9
US-10-414-186-2
(S-10-414-186-2
; Sequence 2, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
FILE REFERENCE: 98-55C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. US20030148447Alak, Julia
APPLICANT: Hammond, Angela K.
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                                                                                                                                               PLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQAS
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RESULT 10
US-10-456-780-6
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN
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CURRENT APPLICATION NUMBER: US/10/414,186
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/99/404,641
PRIOR APPLICATION NUMBER: US/99/404,641
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR FILING DATE: EARLIER FILING DATE: US
PRIOR FILING DATE: EARLIER FILING DATE: US
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
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Best Local Similarity
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APPLICANT: No. US20030175825A1Ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
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ORGANISM: Homo
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Pred. No. 2.8e-228;
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Sequence 115, Application US/10659684
Publication No. US20040110932A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond Angela K.
APPLICANT: Hammond Angela K.
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; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-6
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Best Local (
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/659,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: OTHER THERAPEUTIC API
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEO ID NOS: 17
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; ORGANISM: Homo
US-10-659-684-115
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US-10-620-169-4
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                                                                                                                                                                                           Sequence 4, Application US/10620169
Publication No. US20040136954A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows
SEQ ID NO 115
LENGTH: 538
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Best Local Similarity
APPLICANT: Grusby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Voung, Deborah
APPLICANT: Collins, Mary
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
TITLE OF INVENTION: Cell bevelopment and Function
FILE REFERENCE: 22058-585
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15
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PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR PILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
NUMBER OF SEQ ID NOS: 115
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APPLICANT: PROBERIAL, SCOTT R.
APPLICANT: CONKLIN, DARRELL C.
APPLICANT: NOVAK, JULIA E.
APPLICANT: HOVAK, JULIA E.
APPLICANT: HOWAK, JULIA E.
APPLICANT: HARMOND, ANGELA K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/10/715,998
CURRENT FILING DATE: 2003-11-18
FRIOR APPLICATION NUMBER: US/10/414,186
PRIOR FILING DATE: 2003-04-14
PRIOR FILING DATE: 2003-04-14
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/
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US-10-620-169-4
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
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Best Local Similarity
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PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/403,001
PRIOR FILING DATE: 2002-08-12
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        60/123,546
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Sequence 2, Application US/10872087

Publication No. US20040235743A1

GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Nelly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECFILE REFERENCE: 00-22D1

CURRENT APPLICATION NUMBER: US/10/872,087

CURRENT APPLICATION NUMBER: US 60/194,731

PRIOR FILING DATE: 2000-04-05

PRIOR PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: US 69/825,561

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03
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; ORGANISM: Homo
US-10-715-998-2
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US-10-872-087-2
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
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GENERAL INFORMATION:

APPLICANT: Pressell, Scott R.

APPLICANT: Pressell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Byrescher, Cindy A.

APPLICANT: Hoolter, Donald C.

APPLICANT: Hoolter, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holson, Janet V.

APPLICANT: Holson, Andrew J.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LICETICATION NUMBER: US/10/787,442

CURRENT APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-2
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Pred. No. 2.8e-228;
); Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Ve
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                             LELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGG
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EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
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Search completed: September 7, 2006, 12:57:58
Job time: 197.717 secs

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  Query
Match
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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2958
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Maximum Match 100%
Listing first 45 summaries
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           US-10-806-611-6
US-10-669-920-305
US-10-669-920-302
US-10-669-920-285
US-10-669-920-287
US-10-669-920-287
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US-10-669-920-297
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US-10-669-920-297
US-10-569-920-293
US-10-569-920-293
US-10-569-920-293
US-10-505-928-650
US-10-505-928-650
US-10-505-928-650
US-10-511-347-379-4
US-11-344-379-4
US-10-548-727-10
US-10-548-727-10
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Sequence 305, App
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Sequence 285, App
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Sequence 2426, App
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ა. 8	3.9	3.9	3.9	3.9	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.2	4.3	4.6	4.8	4.9	4.9
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US-11-314-257-2	US-11-056-355B-64206	US-10-953-349-32681	US-11-056-355B-64207	US-10-953-349-32682	US-11-313-104-16	US-10-511-937-2988	US-11-300-928-27	US-11-296-155-32	US-11-296-092-32	US-11-247-437-14	US-11-194-051-23	US-11-194-051-22	US-10-669-920-520	US-10-669-920-1407	US-10-519-342-3	US-11-312-958-56	US-10-511-937-2966	US-11-297-957-2	US-10-511-937-2465
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
2, Appli	64206, A	32681, A	64207, A	32682, A	16, Appl	2988, Ap	27, Appl	•	32, App1	14, Appl	23, Appl	•	520, App	1407, Ap	3, Appli	56, Appl	2966, Ap	2, Appli	

ALIGNMENTS

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; SEQ ID NO 6; LENGTH: 538; TYPE: PRT; ORGANISM: Homo sapiens US-10-806-611-6
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US-10-806-611-6
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Publication No. US20060159855A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Collins, Mary
APPLICANT: Senices, Mayra
APPLICANT: OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
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Best Local
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CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOPTWARE: Patentin version 3.2
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                                          241
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                                                                                                                                                                                                 121 APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                                                                                                                                            61 EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
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                                                                                                                RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                        APPFNYTYTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                   RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS
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CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
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US-10-669-920-305
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Best Local S
Matches 536
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SEQ ID NO 305
LENGTH: 536
TYPE: PRT
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APPLICANT: Malandro,
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TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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LLLLVIVFIPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSS 300
                                      RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                             RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                               APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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                                                                                                                     APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
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b. US20060194265A1
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Pred. No. 7.2e-230;
0; Mismatches 0;
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RESULT 3
US-10-669-920-307
US-10-669-920-307
Sequence 307, Applicat
Publication No. US2000
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR PILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR APPLICATION NUMBER: US 10/032,281
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
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SEQ ID NO 307
LENGTH: 536
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
NUMBER OF SEQ ID NOS: 1441
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APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
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                                                            APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDS
                                                                                                                                         EATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKP
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Pred. No. 7.2e-230;
0; Mismatches 0;
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APPLICANT: Collins, Mary
APPLICANT: Collins, Mary
APPLICANT: Senices, Mayra
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 529
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-8
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US-10-806-611-8
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Best Local S
Matches 340
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SLELGPWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFW---PTAQ 356
                                                                                  LLLLVIVFIPAFWSLKTHPLWRKHWKKIWA-VPSPERFFMPLYKGCSGDFKKWVGAPFTGS
                                                                                                                                                              RSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL
                                                                                                                                                                                                                                                                                                                                                                           MPRGPVAALLLILHGAWSCLDLTCYTDYLWTITCVLETRSPNPSILSLTWQDEYEBIQD
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                                                           LLAVLIIVL-VFMGLKIHLPWRLWKKIWAPVPTPESFFQPLYREHSGNFKKWVNTPFTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.7%; Score 1735.5; DB 6; Length flarity 62.7%; Pred. No. 1.6e-132; Conservative 49; Mismatches 136; Indels
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PRIOR APPLICATION NUMBER: US 10/322,696;
PRIOR FILING DATE: 2002-12-17;
NUMBER OF SEQ ID NOS: 1441;
SOFTWARE: FastSEQ for Windows Version 4.;
SEQ ID NO 302;
LENGTH: 579;
TYPE: PRT
ORGANISM: Mus musculus
US-10-669-920-302
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US-10-669-920-302
Sequence 302, Applica
Publication No. US200
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR APPLICATION NUMBER: US 99/997,722
PRIOR FILING DATE: 2001-11-00
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR APPLICATION NUMBER: US 10/082,281
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR FILING DATE: 2002-12-17
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Best Local Similarity
Matches 340; Conserv
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APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
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                                                                                                                                                   111 QETFCSLHRSGHNTTHIWYTCHMRLSQFLSDEVFIVNVTDQSGNNSQECGSFVLAESIKD
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PRIOR FILING DATE: 2001-10-23
PRIOR PELICATION NUMBER: US 10/052,482
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR PILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/087,192
                                                                                                                                                                       Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                            SEQ ID NO 285
LENGTH: 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
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SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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ALQD--TSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLC 110
                                           ELKDEATSCSLH----RSAHNAT------HATYTCHM-----DVFHFMADDIFSVNITD 100
                                                                                                                              WAAPLILLI--LQGGW-----GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAGSPLAGLDMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPPPLSSPGPQ 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLIDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPPLADGEDWAGGLPWGGRSPGGVSES 476
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                                                                                      WRLPLIILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS--
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o. US20060194265A1
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                                                                                                                                                                       9.6%; Score 284; DB 6; Length 549;
26.1%; Pred. No. 5.6e-15;
7ative 73; Mismatches 201; Indels 114;
                                                                                                                                                                       Gaps
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PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR APPLICATION NUMBER: US 10/322,281
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SEQ ID NO 287
LENGTH: 549
TYPE: PRT
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                                                                                                                                Matches
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/322,281 PRIOR FILING DATE: 2002-12-17 PRIOR APPLICATION NUMBER: US 10/322,696 PRIOR FILING DATE: 2002-12-17
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APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 10/004,113 PRIOR FILING DATE: 2001-10-23
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  ELKDEATSCSLH----RSAHNAT-----HATYTCHM-----DVFHFMADDIFSVNITD 100
                                           WRLPLLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS------QDG
                                                                                     WAAPLLLL--LQGGW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPC 388
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                                                                                                                                Conservative
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                                                                                                                              9.6%; Score 284; DB 6;
26.1%; Pred. No. 5.6e-15;
ative 73; Mismatches 201
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                                                                                     GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 56
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                                                                                                                                                                      Length 549
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PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR TILING DATE: 2001-11-30
PRIOR PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
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                                                                     Matches
                                                                                          Best Local
                                                                                                            Query Match
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APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 10/322,696 PRIOR FILING DATE: 2002-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 20366-066001
                                                                                                                                                                                 ORGANISM: Mus
                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 10/322,281 FILING DATE: 2002-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 RTLSPGHTWEEAP---LLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEF--TTWSPWS
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                                                                     138;
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5 WAAPL--LLLLLQGGW------GCPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYE 56
                                                                                          Similarity
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p. US20060194265A1
                                                                     Conservative
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                                                                                                                                                                                                                                                                  for Windows Version
                                                                8.1%; Score 240.5; DB 6; 23.6%; Pred. No. 1.8e-11; tive 64; Mismatches 198;
                                                                   Indels
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                                                                                                              537;
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                                                                   Gaps
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                                                                     ) ORGANISM: Homo US-10-511-937-2426
                                                                                                            PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2426
LENGTH: 508
TYPE: PRT
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2426, Application US/10511937 Publication No. US20060088836A1
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                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woodward, Robert
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  7.2%;
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  Score 213; DB 6;
Pred. No. 2.9e-09;
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NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 292
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 10/034,650 PRIOR FILING DATE: 2001-12-20 PRIOR APPLICATION NUMBER: US 10/085,117 PRIOR FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS FILE REFERENCE: 20366-066001
                                                          PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morris, David W. APPLICANT: Malandro, Marc
                                                                                                    APPLICATION NUMBER: US 10/322,281 FILING DATE: 2002-12-17
                                                                                                                                             APPLICATION NUMBER: US 10/087,192 FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                           FILING DATE: 2001-11-08
APPLICATION NUMBER: US 09/997,722
                                                                                                                                                                                                                                                                            FILING DATE: 2001-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 QSGNYSQECGSFLLAESIKPAPPFNVTVTF-------SGQYNISWRSD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 STLTLTWODQYEELKDEATS-CSLHRSAHNATHATYTCHM----DVFHFMADDIFSVNITD 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EASSCSSALA---SKPSPEGASAASFEYTILDPSSQLLRPWTLCPELPP 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGSDCSSPVECDFTSPGDEG-----PPRSYLRQWVVIP--PP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D----PPAS-----LEVLSERC------WGTMQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVYSCHPPRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLV 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLL--LLLLVIVFIPAFWSLKTHP 259
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; TYPE: PRT
; ORGANISM: Mus r
US-10-669-920-292
                                                        APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN
FILE REPERENCE: 2036-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/52,482
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR APPLICATION NUMBER: US 10/085,117
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FILING DATE: 2002-02-2
APPLICATION NUMBER: US
FILING DATE: 2002-03-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPAFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGPWSP 308
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                                         2002-02-27
      2002-03-01
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Pred. No. 5.9e-09;
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RESULT 12
US-10-669-920-299
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; ORGANISM: Homo sapiens
US-10-669-920-297
              Sequence 299, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: MOSTIS, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
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PRIOR PILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 10/004,113
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Local Similarity 22.9%;
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                                                                                                                                                                                                                                                                    764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 QIPVPDPATHGQY------IVSV----QPRRAEKHIKS---SVNIQMAPP-SL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 DLVCYTDYLQTVICILEMWNLHPSTLT--LTWQDQYEELKDEATSC-----SLHRSAH- 72
                                                                                                                                                                                                                                                                    YVELPPIEGRSPRSPRNNPVP 784
                                                                                                                                                                                                                                                                                                          WVVIPP-----PLSSPGP 535
                                                                                                                                                                                                                                                                                                                                                                                    FVGSDCSSPVECDFT------
                                                                                                                                                                                                                                                                                                                                                                                                                    AAGS-----PSLESG------ĠĠ₽A₽PALGPRVĠĠQDQKDSPVAIPMSSGĎTEĎPĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLVIVFIP-AFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKW----VGAP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVTKDGDSYSLRWETMKMRYEHIDHTF-----EIQYRKDTATWKDSKTETL--QNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPDILGQPEPPQEGGSQKSPPPGSLEYLCLPAGGQVQLVPLAQAMGPGQAVEVERRPSQG
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                                                                                                                                                                                                                                                                                                                                              -VASGYVSSADLVFTPNSGASSVSLVPSLGLPSDQTPSLCPGLASGPPGAPGPVKSGFEG
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Pred. No. 2.2e-08;
6; Mismatches 225; Indels 188;
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                                                                          CANCER
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PRIOR FILING
PRIOR APPLICATION NUMBER: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 117
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; ORGANISM: Homo sapiens
US-10-669-920-299
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PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FREUSEQ for Windows Version 4
SEQ ID NO 299
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PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 NVTKDGDSYSLRWETMKMRYEHIDHTF-----EIQYRKDTATWKDSKTETL--QNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 NLECFFDGAAVLSCSWEVRKEVASSVSFGLFYKPSPDAGEEECSPVLREGLGSLHTRHHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DLVCYTDYLQTVICILEMWNLHPSTLT--LTWQDQYEELKDEATSC-----SLHRSAH- 72
                                                                                                                                                                                                                   PLGSLLDRLKPPLADGEDWAGGLPWGGRSP-----GGVSESEAGSPLAGLDMDTFDSG
                                                                                                                                                                                                                                                              LPDILGQPEPPQEGGSQKSPPPGSLEYLCLPAGGQVQLVPLAQAMGPGQAVEVERRPSQG
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                                           WVVIPP-----PLSSPGP 535
                                                                                                                                                                            AAGS-----PSLESG-----
                                                                                                                                                                                                                                                                                                       CEDD-GYPALDLDAGLEPSP---GLEDPLLDAGTTVLSCGCVSAGSPGLG-----G
                                                                                                                                                                                                                                                                                                                                                     EQPPSPQPGPPAASHTPEKQASS--------FDFNGPYLGPPHSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGSPPHQGPWGSRFPELEGVFPVGFGDSEVSPLTIEDPKHVCDPPSGPDTTPAASDLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFLTIAVLLALRFCGIYGYRLRRKWEEKIPNPSKSHLFQ-----NGSAELWPPGSMSAF
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YVELPPIEGRSPRSPRNNPVP
                                                                                                                                FVGSDCSSPVECDFT-----
                                                                                    -VASGYVSSADLVFTPNSGASSVSLVPSLGLPSDQTPSLCPGLASGPPGAPGPVKSGFEG
                                                                                                                                                                                                                                                                                                                                                                                                 PAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEGPCTWP---CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTGSSLELGPWS---PEV-----PSTLE--VYSCHPPRSPAKRLQLTELQE
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; Pred. No. 2.2e-08;
66; Mismatches 225
  784
                                                                                                                                                                            -GGPAPPALGPRVGGQDQKDSPVAIPMSSGDTEDPG
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                                                                                                                                ----SPGDEGPPRSYLRQ 522
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392

343

304

447

561

336 501

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440 599 393

493

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RESULT

US-10-669-920-295

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; ORGANISM: Homo sapiens
US-10-669-920-295
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CURRENT APPLICATION NUMBER: US/10/669,920

CURRENT FILING DATE: 2003-09-23

PRIOR APPLICATION NUMBER: US 10/004,113

PRIOR FILING DATE: 2001-10-23

PRIOR PILING DATE: 2001-11-23

PRIOR PILING DATE: 2001-11-30

PRIOR PILING DATE: 2001-11-30

PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: US 10/034,650

PRIOR PILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: US 10/034,650

PRIOR PILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: US 10/085,117

PRIOR PILING DATE: 2002-02-27

PRIOR FILING DATE: 2002-02-27

PRIOR FILING DATE: 2002-02-27

PRIOR FILING DATE: 2002-02-27

PRIOR FILING DATE: 2002-02-27
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 295
LENGTH: 901
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TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%; Score 204.5; DB 6; Local Similarity 23.7%; Pred. No. 2.9e-08; les 121; Conservative 51; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 10/322,696
FILING DATE: 2002-12-17
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FILING DATE: 2002-03-01
APPLICATION NUMBER: US 10/322,281
FILING DATE: 2002-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 LPMWVLALIVIFLTIAVLLALRFCGIYGYRLRRKWEEKIPNPSKSHLFQ-----NGSAE 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 NIQMAPP-SLNVTKDGDSYSLRWETMKMRYEHIDHTF-----EIQYRKDTATWKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 SIKPAPPFNVTVTFSG-QYNISW-----RSDYEDPAFYMLKGKLQYELQYRNRGDPWAVS 170
                                                                                             701 MSSGDTEDPG-VASGYVSSADLVFTPNSGASSVSLVPSLGLPSDQTPSLCPGLASGPPGA 759
                                           EGPPRSYLROWVVIPP-----PLSSPGP 535
                                                                                                                                           GLDMDTFDSGFVGSDCSSPVECDFT------SPGD 512
                                                                                                                                                                                           VEVERRPSQGAAGS-----PSLESG------GGPAPPALGPRVGGQDQKDSPVAIP 700
                                                                                                                                                                                                                                                                                                                                                                                         TTPAASDLPTEQPPSPQPGPPAASHTPEKQASS-----FDFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWPPGSMSAFTSGSPPHQGPWGSRFPELEGVFPVGFGDSEVSPLTIEDPKHVCDPPSGPD 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KW----VGAPFTGSSLELGPWS---PEV------PSTLE--VYSCHPPRSPA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEGWNPHLLLLLLLVIVFIP-AFWSLKTHPLWRLWKKIWAVPSPERFFMPLYKGCSGDFK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTETL--QNAHSMALPALE--PSTRYWARVRV-RTSRTGYNGIWSEWSEARSWDTES--V
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PGPVKSGFEGYVELPPIEGRSPRSPRNNPVP 790
                                                                                                                                                                                                                                           -----GPLGSLLDRLKPPLADGEDWAGGLPWGGRSP-----GGVSESEAGSPLA 483
                                                                                                                                                                                                                                                                                                                                         PCTWP----CSCEDD-GYPALDLDAGLEPSP---GLEDPLLDAGTTVLSCGCVSAGSPGLG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                       KRLQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG 386
                                                                                                                                                                                                                                                                                         PYLGPPHSRSLPDILGQPEPPQEGGSQKSPPPGSLEYLCLPAGGQVQLVPLAQAMGPGQA 655
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 161; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 TLTWQDQYEELKDEATSCSLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSYQGTWSEWSDPVIFQTQSEELKEGWNPHLLLLLLLVIVFIPAFWSLKTHPLWRLWKKI 267
AGYKAF-SSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPAP------VP
                                                                                           TVPQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGE
                                                                                                                                                                                           NLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                         AELVESDGV--PKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTV-LDAEG-----
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                                             -DMDTFDSGFVGSDCSSPVECDFTS-----
                                                                                                                                                   --PLADGEDW----
                                                                                                                                                                                                                                              ----LEDPLIDAGTTV---LSCGCVSAGSPGLGGP---LGSLLDRLKP------
                                                                                                                                                                                                                                                                                              QDMGESCLLPPSGSTSAHMPWDEFPS----AGPKEAPPWGKEQPLHLEPSPPASPTQSPD 480
                                                                                                                                                                                                                                                                                                                                         -----PCTWPCSCED-----DGYPALDLDAG------LEPSPG-----
                                                                                                                                                                                                                                                                                                                                                                                         VECEEEEEVEEEKGSFCASPESSRDD-FQEGRE---GIVARLTESLFLDLLGEENGGFCQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPHKAAKEMPFQGSG--KSAWCPVEISKTVLWPESISVVRC-----VELFEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFLLAESIKPAPPFNVTV--TFSGQYNISWRSDYEDPAFYMLKGKLQY
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APPLICANT: LY. NGOC
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612001014
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-3001
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US-10-511-937-3001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.5%; Score 193.5; DB 6; Length 825; Best Local Similarity 21.8%; Pred. No. 2e-07; Matches 161; Conservative 69; Mismatches 220; Indels 289;
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
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                                                                                                                                                                                                                                                                   206 OCYNTTWSEWSPSTKWH---NSYREPFEQHLLLGVSVSCIVILAVCLLCYVSITKIKKEW 262
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  369
                                          338 AELVESDGV--PKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTV-LDAEG----- 386
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Fry, Kirk
Woodward, Robert
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Db 650 V	Оу 528 РІ	Db 601 A		Qy 486 -I					
650 VPLFTFGLDREPPRSPOSS 668	PPLSSPGPQAS 538	601 AGYKAF-SSILASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPAP		486 -DMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLRQWVVIP 527	PTSGYQEFV	452PLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGL	481 NLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELGPDPLLARHLEEVEPEMPCVPQLSEPT 540 452PLADGEDW	LEDPLLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKP	425 QDMGESCLLPPSGSTSAHMPWDEFPSÄGPKEAPPWGKEQPLHLEPSPASPTQSPD 480 414LEDPLLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKP
		VP 649	WVIP 527		3PPGE 600	3PPGE 600	SEPT 540	LSEPT 540 485 3PPGE 600	IQSPD 480 451 LSEPT 540 485 3PPGE 600

Search completed: September 7, 2006, 12:58:47 Job time : 36.0486 secs

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